



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 197922

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Monday, August 14, 2006
Case Serial Number: 10/764212

From: Vira David
Location: Biotech-Chem Library
REM-1A41
Phone: (571)272-1972

Virajita.David@uspto.gov

Search Notes

Examiner Portner,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David
Intern
STIC Biotech/Chem Library
(571)272-1972



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library, Remsen Bldg.



STIC-Biotech/ChemLib

197922

From: Portner, Ginny
Sent: Tuesday, August 08, 2006 12:54 PM
To: STIC-Biotech/ChemLib
Subject: 10/764,212

please search sequences 16, 18 and 20, and oligomer search with respect to amino acid sequences

Ginny Portner
Remsen Building
Art Unit 1645
Room E03, B02; Mail Box 3C18
(571) 272-0862

8/8/2006

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:30:38 / Search time 117.648 Seconds
(without alignments)
1733.289 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 2388
Sequence: 1 MFQPLLDVAVESASIEKMS.....KIRKAYKPKPKPYCAP 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 45716429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2388	100.0	446	9 AEB70145	Aeb70145 Helicobac
2	2081	87.1	464	2 AAWE6008	Aaw6008 Helicobac
3	2073	86.8	501	5 ABG30881	Abg30881 H. pylori
4	2064.5	86.5	454	5 ABG30887	Abg30887 H. pylori
5	2058.5	86.2	476	5 ABG30884	Abg30884 H. pylori
6	2050.5	85.9	479	5 ABG30886	Abg30886 H. pylori
7	2040.5	85.4	485	8 ADJ77814	Adj77814 Helicobac
8	2040.5	85.4	485	8 ADJ77349	Adj77349 Alpha-1,3
9	2040.5	85.4	485	8 AEB70135	Aeb70135 Helicobac
10	2036	85.3	486	8 ADJ77810	Adj77810 Helicobac
11	2036	85.3	486	8 ADJ77345	Adj77345 Alpha-1,3
12	2036	85.3	486	8 AEB70131	Aeb70131 Helicobac
13	2026	84.8	485	5 ABG30882	Abg30882 H. pylori
14	1972.5	82.6	425	8 ADJ77820	Adj77820 Helicobac
15	1972.5	82.6	425	8 ADJ77355	Adj77355 Alpha-1,3
16	1972.5	82.6	425	5 AEB70141	Aeb70141 Helicobac
17	1957	82.0	424	5 ABG30885	Abg30885 H. pylori
18	1935.5	79.1	418	5 ABUS2257	Abus2257 Helicobac
19	1894.5	79.3	432	8 ADJ77812	Adj77812 Helicobac
20	1894.5	79.3	432	8 ADJ77347	Adj77347 Alpha-1,3
21	1894.5	79.3	432	8 AEB70133	Aeb70133 Helicobac
22	1861	77.9	440	9 AEB70147	Aeb70147 Helicobac
23	1846	77.3	440	5 ABG30883	Abg30883 H. pylori

24	1815	76.0	391	9 AEB70195	Aeb70195 H. pylori
25	1812.5	75.9	456	9 AEB70149	Aeb70149 Helicobac
26	1804	75.5	377	9 AEB70197	Aeb70197 H. pylori
27	1192	49.9	277	8 ADJ77816	Adj77816 Helicobac
28	1192	49.9	277	8 ADJ77351	Adj77351 Alpha-1,3
29	1192	49.9	277	8 AEB70137	Aeb70137 Helicobac
30	1191	49.9	246	9 AEB70204	Aeb70204 H. pylori
31	1187	49.7	246	9 AEB70203	Aeb70203 H. pylori
32	1183.5	49.6	247	9 AEB70202	Aeb70202 H. pylori
33	1142	47.8	256	9 AEB70199	Aeb70199 H. pylori
34	1122	47.0	231	9 AEB70193	Aeb70193 H. pylori
35	1111	46.5	250	9 AEB70206	Aeb70206 Helicobac
36	1099.5	46.0	245	9 AEB70201	Aeb70201 H. pylori
37	1049.5	43.9	247	9 AEB70205	Aeb70205 H. pylori
38	1008	42.2	559	9 AEB70211	Aeb70211 Helicobac
39	975	40.8	227	9 AEB70154	Aeb70154 H. pylori
40	956	40.0	545	9 AEB70212	Aeb70212 Helicobac
41	685.5	28.7	146	5 ABUS1720	Abus1720 Helicobac
42	562	23.5	169	5 ABUS1151	Abus1151 Helicobac
43	531	22.2	130	5 ABUS1509	Abus1509 Helicobac
44	527	22.1	119	9 AEB70177	Aeb70177 H. pylori
45	494	20.7	124	5 ABUS1153	Abus1153 Helicobac

ALIGNMENTS

RESULT 1	
ID AEB70145	standard; protein; 446 AA.
XX	
AC AEB70145;	
XX	
DT 06-OCT-2005	(first entry)
XX	
DE Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 16.	
XX	
KW Fucosyltransferase; protein production; enzyme.	
XX	
OS Helicobacter pylori; strain 1111.	
XX	
FH Key	Location/Qualifiers
FT	Misc-difference 168
FT	/note= "Encoded by GC"
FT	Misc-difference 355
FT	/note= "Encoded by AG"
FT	Misc-difference 408
FT	/note= "Encoded by AG"
FT	Misc-difference 435
FT	/note= "Encoded by AG"
XX	
PN US2005164338-A1.	
XX	
PD 28-JUL-2005.	
XX	
PP 22-JAN-2004; 2004US-00764212.	
XX	
PR 22-JAN-2004; 2004US-00764212.	
XX	
PA (NEOS-) NEOSE TECHNOLOGIES INC.	
XX	
PI (UTAL-) UNIV ALBERTA.	
XX	
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ,	
XX	
DR WPI; 2005-521417/53.	
XX	
DR N-PSDB; AEB70144.	
XX	
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful	
XX	
PS for synthesizing oligosaccharides, glycoproteins, or glycolipids.	
XX	
PS Claim 1; SEQ ID NO 16; 97pp; English.	
XX	
CC The present invention provides alpha-1,3/4-fucosyltransferase (also	

CC termed as fucosyltransferase) proteins and nucleic acids from various
 CC strains of *Helicobacter pylori*. This enzyme catalyzes the transfer of a
 CC fucose residue from a donor substrate to an acceptor substrate. The
 CC fucosyltransferase polynucleotides and polypeptides are useful for the
 CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
 CC sequence is *Helicobacter pylori* fucosyltransferase protein.

XX Sequence 446 AA:

Query Match 100.0%; Score 2388; DB 9; Length 446;
 Best Local Similarity 100.0%; Pred. No. 3.6e-201;
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWMDDEIKERKSVLYRIFSORYITAAH 60
D 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWMDDEIKERKSVLYRIFSORYITAAH 60
QY 61 QNPNEFSDLVFSPNPLGSAKILSYONAKRVFTYGENSVPNFLPDYVIGFDELDFRDRYL 120
D 61 QNPNEFSDLVFSPNPLGSAKILSYONAKRVFTYGENSVPNFLPDYVIGFDELDFRDRYL 120
QY 121 RMPLYYDRLHKAESVNDTTSPPYKLDKNSLYTLAKPSHQFKENHPNLCVAVNDESDPLKR 180
D 121 RMPLYYDRLHKAESVNDTTSPPYKLDKNSLYTLAKPSHQFKENHPNLCVAVNDESDPLKR 180
QY 181 GVSFVSANANAPMNAFYDALNSIEPVYGGGVKNTLGYNVKNKSEPLSQYKFNLCFEN 240
D 181 GVSFVSANANAPMNAFYDALNSIEPVYGGGVKNTLGYNVKNKSEPLSQYKFNLCFEN 240
QY 241 SQGYYVTEKILDAFSTHPIRYMGSPSYAKDPNPEKPNVNDENNPDALDIYIKYLAH 300
D 241 SQGYYVTEKILDAFSTHPIRYMGSPSYAKDPNPEKPNVNDENNPDALDIYIKYLAH 300
QY 301 PNAYLDMLYENPLALDGKAYFYODLSFPKKILAFKTLLENPTLYHKSSTSPWMECDLDE 360
D 301 PNAYLDMLYENPLALDGKAYFYODLSFPKKILAFKTLLENPTLYHKSSTSPWMECDLDE 360
QY 361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL 420
D 361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL 420
QY 421 SQNTSFKIRKRAYOKPIKMPYPCAP 446
D 421 SQNTSFKIRKRAYOKPIKMPYPCAP 446
  
```

RESULT 2
 ID AAW86008 standard; protein; 464 AA.
 XX AAW86008;
 AC
 DT 17-OCT-2003 (revised)
 DT 29-MAR-1999 (first entry)
 XX
 DE *Helicobacter pylori* alpha-1,3-fucosyltransferase.
 XX
 KW Alpha-1,3-fucosyltransferase; fuct gene; Lewis X; Lewis Y;
 KW sialyl Lewis X; tumour associated antigen; cancer; infection;
 KW mucosal disease; diagnosis; fucosylated oligosaccharide.
 XX
 OS *Helicobacter pylori*; strain NCTC 11639.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 96..99 /note="Asn is N-glycosylated"
 FT Modified-site 137..139 /note="Asn is N-glycosylated"
 FT Modified-site 332..334 /note="Asn is N-glycosylated"
 FT Modified-site 341..343 /note="Asn is N-glycosylated"
 FT Peptide 364..370 /note="Asn is N-glycosylated"

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FT Peptide /note="peptide repeat"
FT 371..377
FT Peptide /note="peptide repeat"
FT 378..384
FT Peptide /note="peptide repeat"
FT 385..391
FT Peptide /note="peptide repeat"
FT 392..398
FT Peptide /note="peptide repeat"
FT 399..405
FT Peptide /note="peptide repeat"
FT 406..412
FT Peptide /note="peptide repeat"
FT 413..419
FT Peptide /note="peptide repeat"
FT 435..437
FT Modified-site /note="Asn is N-glycosylated"
  
```

MO9855630-A2.
 10-DEC-1998.
 05-JUN-1998; 98WC-CA000564.
 06-JUN-1997; 97US-0048857P.
 (UYAL-) UNIV ALBERTA.
 Taylor DE, Ge Z;
 WPI, 1999-059913/05.
 DR N-PSDB; AAW80321.
 XX
 PT New isolated alpha-1,3-fucosyltransferase gene - obtained from
 PT *Helicobacter pylori*, used to develop products for the diagnosis and
 PT treatment of intestinal mucosal diseases, e.g. tumours.
 XX
 PS Claim 6; Fig 2; sipp; English.
 XX
 CC This is the amino acid sequence of the novel alpha-1,3-
 CC fucosyltransferase of *Helicobacter pylori* NCTC 11639, as deduced from the
 CC newly isolated fuct gene (see AAW80321). The enzyme is characterised by 8
 CC C-terminal heptad repeats and by the lack of a transmembrane domain. The
 CC absence of a transmembrane domain allows the enzyme to be readily
 CC released from recombinant host cells. The enzyme can be used in the
 CC production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
 CC sialyl Lewis X, which are structurally similar to certain tumour
 CC associated antigens found in mammals. These glycoconjugates also have
 CC research and diagnosis utility in the development of assays to detect
 CC mammalian tumours. The enzyme can also be used to raise specific
 CC antibodies. Inhibition of abnormal fuct gene product activity can be used
 CC for the treatment of intestinal mucosal disease. (Updated on 17-OCT-2003
 CC to standardise OS field)
 XX
 SQ Sequence 464 AA:

Query Match 87.1%; Score 2081; DB 2; Length 464;
 Best Local Similarity 87.1%; Pred. No. 3.9e-174;
 Matches 393; Conservative 15; Mismatches 27; Indels 16; Gaps 2;

```

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWMDDEIKERKSVLYRIFSORYITAAH 60
D 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWMDDEIKERKSVLYRIFSORYITAAH 60
QY 61 QNPNEFSDLVFSPNPLGSAKILSYONAKRVFTYGENSVPNFLPDYVIGFDELDFRDRYL 120
D 61 QNPNEFSDLVFSPNPLGSAKILSYONAKRVFTYGENSVPNFLPDYVIGFDELDFRDRYL 120
QY 121 RMPLYYDRLHKAESVNDTTSPPYKLDKNSLYTLAKPSHQFKENHPNLCVAVNDESDPLKR 180
D 121 RMPLYYDRLHKAESVNDTTSPPYKLDKNSLYTLAKPSHQFKENHPNLCVAVNDESDPLKR 180
QY 181 GVSFVSANANAPMNAFYDALNSIEPVYGGGVKNTLGYNVKNKSEPLSQYKFNLCFEN 240
  
```

Db	181	GFASPVASNPAPRINAPAFDALNLSIEPVTGGGSVRATLGLYNAVKNKEFLRQYKFNCFEN	240
Qy	241	SQGGVYVTEKILDAFSSHITIPLYMGSPSTAXDPNPGFVNVNDPNNPDAIDYIKTLATH	300
Db	241	TGGGIVYVEKILDAFSSHITIPLYMGSPSAKQPNPSPFVNVHDFKNFDEAIDYIKTLATH	300
Qy	301	PNAYILDMLYENEPNALDGRAYFYQDLSFFKILAFKFTILENDITVYHKSSTSEFWECEDLE	360
Db	301	KNAVYIDMLYENPDLNLTLDGRAYFYQNLSPFKILAFKFTILENDITVYH--DNPFIFCRDLNLS	358
Qy	361	PLASIIDDLRV-----NYDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVY	406
Db	359	PLVITIDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVYDDLNAVY	418
Qy	407	YERLIQNAPSPLIEESQNTSFKYIKRAYQCPY	437
Db	419	YERLISKATPPLIESQNTTSKYIKRAYQKSL	449

XX	RESULT 3
XX	ID AEG30881
XX	AEG30881 standard; protein; 501 AA.
AC	
XX	AEG30881;
DT	21-OCT-2002 (first entry)
XX	
DE	H. pylori alpha,3 fucosyltransferase #1.
KM	Enzyme; fuct; alpha,3 fucosyltransferase; oligosaccharide; lex; Ley;
XX	slex; Helicobacter pylori infection; malignant cell; mammalian tumour
OS	Helicobacter pylori.
XX	
Key	Location/Qualifiers
FH	Misc-difference 53
FT	/note= "Encoded by CA"
FT	Misc-difference 145
FT	/note= "Encoded by ACTC"
FT	Misc-difference 214
FT	/note= "Encoded by CTG"
FT	Misc-difference 264
FT	/note= "Encoded by TGG"
FT	Misc-difference 269
FT	/note= "Encoded by CTC"
FT	Misc-difference 272
FT	/note= "Encoded by AT"
FT	Misc-difference 278
FT	/note= "Encoded by GT"
FT	465..501
Region	/note= "Region not encoded by sequence appearing as ABK89249"
XX	
PN	US2002068347-A1.
XX	
PD	06-JUN-2002.
XX	
PP	07-DEC-2000; 2000US-00733524.
XX	
PR	05-JUN-1998; 98US-00092315.
XX	
PA	(UYAL-) UNIV ALBERTA.
XX	
PI	Taylor DE, Ge Z;
XX	
DR	WPI, 2002-582480/62.
XX	
N-PSDB;	ABK89249.
PT	Purified transmembrane segment-free alpha,3-fucosyltransferase
PT	polypeptide useful for producing fucosylated oligosaccharides.
XX	
SS	Claim 6; Fig 2A; 37pp; English.

The invention relates a purified transmembrane segment-free alpha 1,3-fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-Ileu-Ala-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn, and X₃ is Leu, Val or Ala. Also included are the nucleic acid encoding the protein (including its complement or fragment), a vector containing the nucleic acid, a host cell containing nucleic acid or vector, an antibody which selectively binds to the protein and a gene expression system for producing transmembrane segment-free alpha₁,3-fucosyltransferase, comprising a host cell modified with the nucleic acid or its enzymatically active portion. The protein and cells are useful for producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by contacting the protein with a substrate such as LacNAc-R and GDP-fucose, and purifying the produced oligosaccharides, or by culturing the cell, contacting the host cell with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alpha₁,3-fucosyltransferase polynucleotide, and detecting hybridisation of the probe; or by amplifying the nucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alpha₁,3-fucosyltransferase-fusion protein, by growing the host cell containing a vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein and isolating the fusion protein. The antibody is useful for detecting the protein in a sample. The presence of the protein in the sample is indicative of infection by *Helicobacter pylori* or the presence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alpha₁,3-fucosyltransferase gene product activity. The nucleic acid is useful as part of ribosome and/or triple helix sequences and for alpha₁,3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents *H. pylori* alpha₁,3-fucosyltransferase encoded by the fucT gene

Query Match	86.8%;	Score 2073;	DB 5;	Length 501;
Best Local Similarity	87.1%;	Pred. No. 2,2e-173;		
Matches 393;	Conservative 15;	Mismatches 27;	Indels 16;	Gaps 2
Qy	1	MFQPLDAAVYESASIEKMASSPPPLKIAVANWMDDEEIKFPKSVLYFISQRYTIAH	60	
Db	1	MFQGLDAAVYESASIEKMASSPPPLKIAVANWMDDEEIKFKNLSVLYFISQRYTILH	60	
Qy	61	QNPNEFSDDLVSNFLGSAKRTILSTONAKRVYTTGENEVPNRLPYAAGFDELDPRDXYL	120	
Db	61	QNPNEFSDDLVSNGNGLGSAKRTILSTONAKRVYTTGENEPPNRLPYAAGFDELDPNDXYL	120	
Qy	121	RMPILYRRLHHKASVNDTTSPYLKKNLSLTIKKPSHQPKENHNLCAYVNDESDDLKR	180	
Db	121	RMPILYRRLHHKASVNDTTA:PYLKKNLSLALKKPSHFCKEKNLCAVYNDESDDLKR	180	
Qy	181	GVVSFVVASNNAPPRNAFYDALNSIEPVTGGSGSVKNTGYNVKNKSEFLSQYKFLCFEN	240	
Db	181	GFASFVASNPPAFIRNAPFYDALNSTIEPVTGGSGSVANTLTGINVKNKNEFLSQYKFLCFEN	240	
Qy	241	SOQGYVTEKILDAVFSHTTIPITYGSPSVADQPNKPEFVNVDHFNPNFEADIDYIKYLTHTH	300	
Db	241	TQSGGYVTEKILDAVFSHTTIPITYGSPSVADQPNKSPVNVNVDHFNQNPBEADIDYIKYLTHTH	300	
Qy	301	PNAYLDMLYENPNALDQKAYFYODLSFKKILAFPTKLTLENDTIYHKSGTSPMECDLDE	360	
Db	301	KNAYLDMLYENPNALDQKAFYONLSFKKILAFPTKLTLENDTIYH--DNPFIIFGRDINE	358	
Qy	361	PLASIDDLRV-----NYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRV	406	
Db	359	PLVYTDILKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRV	418	
Qy	407	YERLLQNASPLPLBSQNTSPFIYKRAYOKPI 437		
Db	419	YERLLSRATPLPLBSQNTTSKIYKRAYOKSL 449		

RESULT 4
ABG30887
XX ABG30887 standard; protein; 454 AA.
AC
XX ABG30887;
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE H. pylori alpha1,3 fucosyltransferase #7.
KM Enzyme; fuct; alpha1,3 fucosyltransferase; oligosaccharide; lex; ley;
XX slex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX
OS Helicobacter pylori; strain 11637.
XX
PN US2002068347-A1.
PD
XX 06-JUN-2002.
XX
PF 07-DEC-2000; 2000US-00733524.
XX
PR 05-JUN-1998; 98US-00092315.
XX
PA (UYAL-) UNIV ALBERTA.
PI Taylor DE, Ge Z;
XX
XX WPI; 2002-582480/62.
DR
XX
PT Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.
XX
PS Example 3; Fig 6; 37pp; English.
XX
XX The invention relates a purified transmembrane segment-free alpha 1,3-
XX fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2-
XX leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
XX Ile, Val or Ala. Also included are the nucleic acid encoding the protein
XX (including its complement or fragment), a vector containing the nucleic
XX acid, a host cell containing nucleic acid or vector, an antibody which
XX selectively binds to the protein and a gene expression system for
XX producing transmembrane segment-free alpha1,3-fucosyltransferase,
XX comprising a host cell modified with the nucleic acid or its
XX enzymatically active portion. The protein and cells are useful for
XX producing fucosylated oligosaccharides, such as lex, ley or slex, by
XX contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
XX and purifying the produced oligosaccharides, or by culturing the cell,
XX contacting the host cell with a substrate, to produce oligosaccharides
XX and purifying the obtained oligosaccharides. The nucleic acid is useful
XX as a probe for detecting the nucleic acid, by contacting a sample with a
XX nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
XX polynucleotide, and detecting hybridisation of the probe; or by
XX amplifying the nucleic acid using polymerase chain reaction (PCR). The
XX host cell is useful for producing a transmembrane segment-free alpha1,3-
XX fucosyltransferase-fusion protein, by growing the host cell containing a
XX vector operably linked to a polynucleotide encoding a desired polypeptide
XX or peptide under conditions which allow expression and secretion of the
XX fusion protein and isolating the fusion protein. The antibody is useful
XX for detecting the protein in a sample. The presence of the protein in the
XX sample is indicative of infection by Helicobacter pylori or the presence
XX of malignant cells. The antibody is also useful for diagnosing disorders
XX and monitoring disease, and for inhibiting abnormal alpha1,3-
XX fucosyltransferase gene product activity. The nucleic acid is useful as
XX part of ribozyme and/or triple helix sequences and for alpha1,3-
XX fucosyltransferase gene regulation. Oligosaccharides synthesised using
XX the protein or cell are useful in the development of assays to detect
XX mammalian tumours. The present sequence represents an H. pylori alpha1,3
XX fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
XX standardise OS field)

SQ Sequence 454 AA;
Query Match 86.5%; Score 2064.5; DB 5; Length 454;
Best Local Similarity 86.3%; Pred. No. 1.1e-172;
Matches 363; Conservative 27; Mismatches 25; Indels 9; Gaps 2;
QY 1 MFQPLLDAAVYASASIEKMAKSPPLKIVANVMWGDDEIKEPKSVLYLFFSQRYTIALH 60
DB 1 MFQPLLDARIESADIEKMAKSPPLKIVANVMWGDDEIKEPKSVLYLFFLSQHYITTLH 60
QY 61 QNPNEFSDLVFSGNPFGSARKILSYQNAKRVFTTGENEVNPNFLFDYALGDELDPEDRYL 120
DB 61 RNPDKRADIVFGNPLGSAKILSYQNTKRIFFYTGENSENPNFLPDYALGDELDPEDRYL 120
QY 121 RNPPLYDRLLHKAESVNDTTPPYKLKDNLSLYTLKKSHPKKNHNPILCAVNDNEPDLK 180
DB 121 RNPPLYDRLLHKAESVNDTTPPYKLKGNLSLYTLKKSHPKKNHNPILCALINNESPLK 180
QY 181 GVVSFVASNANA PMRRAFYDALNSIEPVYGGGSVKNTLGYNVKNKSEFLSQYFNLCFEN 240
DB 181 GPASFVASNANAPMRRAFYDALNSIEPVYGGAVKNTLGYNVKNKSEFLSQYFNLCFEN 240
QY 241 SOGYGVTEKIIDAYFSHTPIYWGSPSYAKDFNPKRFVNVHD FNNDEDAIDYIKYLA TH 300
DB 241 SOGYGVTEKIIDAYFSHTPIYWGSPSYAKDFNPKRFVNVHD FNNDEDAIDYVRYLA TH 300
QY 301 PNAVYDMLTYENPLNALDGKAYFYQDISPKKILAFFTTILENDTITYHKSSTFPMKCDLDE 360
DB 301 PNAVYDMLTYENPLNALDGKAYFYQDISPKKILAFFTTILENDTITYH--NHPFTFYRDLNE 360
QY 361 PLAST-----DDLRVNVYDDL RVNVYDDL RVNVYDDL RVNVYDDL RVNVYDDL RVNVY 413
DB 359 PLVSDINLRINYNDDLRVNVYDDL RVNVYDDL RVNVYDDL RVNVYDDL RVNVYDDL RVNV 418
QY 414 ASPLLELSQNTSFKIYRKAYOKPI 437
DB 419 ASPLLELSQNTSFKIYRKIYOKSL 442
RESULT 5
ABG30884
ID ABG30884 standard; protein; 476 AA.
XX
XX ABG30884;
AC
XX
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
XX H. pylori alpha1,3 fucosyltransferase #4.
DE
XX
XX Enzyme; fuct; alpha1,3 fucosyltransferase; oligosaccharide; lex; ley;
KM slex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX
XX
OS Helicobacter pylori; strain 26695A.
XX
XX
XX US2002068347-A1.
PN
XX
PD 06-JUN-2002.
XX
PF 07-DEC-2000; 2000US-00733524.
XX
PR 05-JUN-1998; 98US-00092315.
XX
XX (UYAL-) UNIV ALBERTA.
PA
XX
XX Taylor DE, Ge Z;
PI
XX
XX WPI; 2002-582480/62.
DR
XX
PT Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.
XX
XX Example 3; Fig 6; 37pp; English.
PS


```
XX Sequence 479 AA;
SQ
Query Match 85.9%; Score 2050.5; DB 5; Length 479;
Best Local Similarity 83.7%; Pred. No. 2e-171;
Matches 390; Conservative 15; Mismatches 30; Indels 31; Gaps 3;

OY 1 MFOPLDAYVESASIERKMAKSPPLKIAVANWMDGEIEKFKSVLYFIFSORYTLAH 60
DB 1 MFOPLDAYVESASIERKMAKSPPLKIAVANWMDGEIEKFKSVLYFIFSORYTLAH 60
OY 61 QNPNEPSDLVFSNPLGSAARKILSYONAKRVFYTGNEVFNFDVAIGFDELDFRDRL 119
DB 61 QNPNEPSDLVFSNPLGSAARKILSYONAKRVFYTGNEVFNFDVAIGFDELDFRDRL 120
OY 120 LRMPLYYDRLLHKKASVNDTTSPYKLKONSLYTLKKSHQFKEHPNICAANNESDPLK 179
DB 121 LRMPLYYDRLLHKKASVNDTTSAPYKLKONSLYALKKPSHFKEHPNICAANNESDPLK 180
OY 180 RGVVSPVANSANAPKRAAFYDALNSIEPTGGGSKVNTLGYVVKKSEFLSQYKFNLCFE 239
DB 181 RGFASFVANSNPAPIRNAFYDALNSIEPTGGGSKVNTLGYVVKKSEFLSQYKFNLCFE 240
OY 240 NSOGGYVTEKILDAYFSHTTPIYWGSPSVAKDPNPKCFVNVHDFNNFDEALDYIKYLHT 299
DB 241 NTQGYVTEKILDAYFSHTTPIYWGSPSVAKDPNPKCFVNVHDFNNFDEALDYIKYLHT 300
OY 300 HPNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIIYHKSSTSPMEECDLD 359
DB 301 HKNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIIYH--DNPFIFRDLANE 358
OY 360 EPLASIDDLRY-----NYDDLRYNVDLRYNVDLRY 391
DB 359 EPLVITIDDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRY 418
OY 392 NYDDLRYNVDLRYNVERLLQNASPLLELSONTSFRTYRKAYOKPI 437
DB 419 NYDDLRYNVDLRYNVERLLQNASPLLELSONTSFRTYRKAYOKSL 464

RESULT 7
ADJ77814 standard; protein; 485 AA.
XX AC ADJ77814;
XX DT 06-MAY-2004 (first entry)
XX DE Helicobacter pylori strain 1218 FutB protein SegID 6.
XX KW PutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
XX KM fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX OS Helicobacter pylori.
XX PN WO2004009838-A2.
XX PD 29-JAN-2004.
XX PF 23-JUL-2003; 2003WO-US023057.
XX PR 23-JUL-2002; 2002US-0398156P.
XX PR 08-NOV-2002; 2002US-0424894P.
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI Johnson KF, Bezila DJ;
XX DR WPI; 2004-123401/12.
XX DR N-PSDB; ADJ77813.
XX PT New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
```

```
PT unglycosylated in its native form or for synthesizing glycolipids.
XX PS Claim 16; SEQ ID NO 6; 72pp; English.
XX CC This invention relates to novel isolated polynucleotides and the encoded
XX CC polypeptides thereof, which are related to the fucosyltransferase enzymes
XX CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
XX CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
XX CC chemically synthesise glycoproteins and glycolipids with the desired
XX CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
XX CC acetylglucosamine), such that they are useful in the preparation of
XX CC glycoconjugates. The present invention describes how bacterial
XX CC fucosyltransferase is unaffected by the sialylation status of the acceptor
XX CC sugar, as opposed to the mammalian homologue, and furthermore,
XX CC bacterially expressed enzymes offer a large cost saving relative to
XX CC mammalian expression systems. This polypeptide sequence is an H. pylori
XX CC strain 1218 FutB protein sequence of the invention.
SQ
Sequence 485 AA;
Query Match 85.4%; Score 2040.5; DB 8; Length 485;
Best Local Similarity 81.6%; Pred. No. 1.5e-170;
Matches 385; Conservative 23; Mismatches 27; Indels 37; Gaps 2;

OY 1 MFOPLDAYVESASIERKMAKSPPLKIAVANWMDGEIEKFKSVLYFIFSORYTLAH 60
DB 1 MFOPLDAYVESASIERKMAKSPPLKIAVANWMDGEIEKFKSVLYFIFSORYTLAH 60
OY 61 QNPNEPSDLVFSNPLGSAARKILSYONAKRVFYTGNEVFNFDVAIGFDELDFRDRL 120
DB 61 QNPNEPSDLVFSNPLGSAARKILSYONAKRVFYTGNEVFNFDVAIGFDELDFRDRL 120
OY 121 RMPLYYDRLLHKKASVNDTTSPYKLKONSLYTLKKSHQFKEHPNICAANNESDPLK 180
DB 121 RMPLYYDRLLHKKASVNDTTSPYKLKONSLYTLKKSHQFKEHPNICAANNESDPLK 180
OY 181 GVVSPVANSANAPKRAAFYDALNSIEPTGGGSKVNTLGYVVKKSEFLSQYKFNLCFE 240
DB 181 GVFASFVANSNPAPIRNAFYDALNSIEPTGGGSKVNTLGYVVKKSEFLSQYKFNLCFE 240
OY 241 NSOGGYVTEKILDAYFSHTTPIYWGSPSVAKDPNPKCFVNVHDFNNFDEALDYIKYLHT 300
DB 241 NSOGGYVTEKILDAYFSHTTPIYWGSPSVAKDPNPKCFVNVHDFNNFDEALDYIKYLHT 300
OY 301 PNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIIYHKSSTSPMEECDLD 360
DB 301 PNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIIYH--DNPFIFRDLANE 358
OY 361 EPLASIDDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYN 393
DB 359 EPLASIDDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYN 418
OY 394 -----DDLRYNVDLRYNVERLLQNASPLLELSONTSFRTYRKAYOKPI 437
DB 419 YDDLRYNVDLRYNVDLRYNVERLLQNASPLLELSONTSFRTYRKAYOKSL 470

RESULT 8
ADJ77349 standard; protein; 485 AA.
XX AC ADJ77349;
XX DT 20-MAY-2004 (first entry)
XX DE Alpha-1,3/4-fucosyltransferase.
XX KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
XX KM fucosyl; fucose.
XX OS Helicobacter pylori; strain 1218 FutB.
XX PN WO2004009793-A2.
```

XX 29-JAN-2004.
PD
XX
PF 23-JUL-2003; 2003MO-US023155.
XX
PR 23-JUL-2002; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Johnson KF, Bezila DJ,
XX WPI; 2004-132958/13.
XX DR N-PSDB; ADJ27348.
XX
PT Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX
PS Claim 1; Fig 3; 84pp; English.
XX
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX
SQ Sequence 485 AA;

Query Match 85.4%; Score 2040.5; DB 8; Length 485;
Best Local Similarity 81.6%; Pred. No. 1.5e-170;
Matches 385; Conservative 23; Mismatches 27; Indels 37; Gaps 2;

QY 1 MFQPLDADAYVESASIERKMAKSPPLKIAVANMWGDEBEIKPKSVLYIFRSQRYTALH 60
DB 1 MFQPLDADAYIESASIERKITSKSPPLKIAVANMWGDEBEVEBFKNILYFLLSQHYTTTLH 60
QY 61 QNPNEPSDLYFNSPLGSAKILSYONAKRVYTTGENEVPNLPDYAIGFDELDFRDRL 120
DB 61 QNPNEPSDLYFGSPISGARKILSYONAKRVYTTGENEVPNLPDYAIGFDELDFRDRL 120
QY 121 RMPLYYDRLLHKAESVNDTTSPYKLKXNSLYTLKKPSHQPKENHPNLCAVNNDESDEPKR 180
DB 121 RMPLYYDRLLHKAESVNDTTSPYKLKXNSLYTLKKPSHQPKENHPNLCAVNNDESDEPKR 180
QY 181 GYVSFVASNANAPRNAPFYDALNSIEPVYGGSVKNTLGVNVKNSBEFLSQYKFNLCFEN 240
DB 181 GFASFVASNPNAPRNAPFYDALNSIEPVYGGSVKNTLGVNVKNSBEFLSQYKFNLCFEN 240
QY 241 SGGYGVVTEKILDAYVSHHTPIYWGSPSAVDNPKPEFVNVDENNDEAIDYKYLAHTH 300
DB 241 SGGYGVVTEKILDAYVSHHTPIYWGSPSAVDNPKPEFVNVDENNDEAIDYKYLAHTH 300
QY 301 PNAYLDMLEPNALDGRKAYFYQDLSFKKILAFPKTILLENDTIYHKSSTSFMMECDLDE 360
DB 301 PNAYLDMLEPNALDGRKAYFYQDLSFKKILAFPKTILLENDTIYH--DNPFIFRYDLNE 358
QY 361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 393
DB 361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 418
QY 394 -----DRLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 437
DB 419 YDRLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 470

RESULT 9
AEB70135
ID AEB70135 standard; protein; 485 AA.

XX AEB70135;
AC
XX
DT 06-OCT-2005 (first entry)
XX
DE Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 6.
XX
KW Fucosyltransferase; protein production; enzyme.
XX
OS Helicobacter pylori; strain 1218.
XX
PN US2005164338-A1.
XX
PD 28-JUL-2005.
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX (UVAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ,
XX WPI; 2005-521417/53.
XX DR N-PSDB; AEB70134.
XX
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Example 1; SEQ ID NO 6; 97pp; English.
XX
CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.
XX
SQ Sequence 485 AA;

Query Match 85.4%; Score 2040.5; DB 9; Length 485;
Best Local Similarity 81.6%; Pred. No. 1.5e-170;
Matches 385; Conservative 23; Mismatches 27; Indels 37; Gaps 2;

QY 1 MFQPLDADAYVESASIERKMAKSPPLKIAVANMWGDEBEIKPKSVLYIFRSQRYTALH 60
DB 1 MFQPLDADAYIESASIERKITSKSPPLKIAVANMWGDEBEVEBFKNILYFLLSQHYTTTLH 60
QY 61 QNPNEPSDLYFNSPLGSAKILSYONAKRVYTTGENEVPNLPDYAIGFDELDFRDRL 120
DB 61 QNPNEPSDLYFGSPISGARKILSYONAKRVYTTGENEVPNLPDYAIGFDELDFRDRL 120
QY 121 RMPLYYDRLLHKAESVNDTTSPYKLKXNSLYTLKKPSHQPKENHPNLCAVNNDESDEPKR 180
DB 121 RMPLYYDRLLHKAESVNDTTSPYKLKXNSLYTLKKPSHQPKENHPNLCAVNNDESDEPKR 180
QY 181 GYVSFVASNANAPRNAPFYDALNSIEPVYGGSVKNTLGVNVKNSBEFLSQYKFNLCFEN 240
DB 181 GFASFVASNPNAPRNAPFYDALNSIEPVYGGSVKNTLGVNVKNSBEFLSQYKFNLCFEN 240
QY 241 SGGYGVVTEKILDAYVSHHTPIYWGSPSAVDNPKPEFVNVDENNDEAIDYKYLAHTH 300
DB 241 SGGYGVVTEKILDAYVSHHTPIYWGSPSAVDNPKPEFVNVDENNDEAIDYKYLAHTH 300
QY 301 PNAYLDMLEPNALDGRKAYFYQDLSFKKILAFPKTILLENDTIYHKSSTSFMMECDLDE 360
DB 301 PNAYLDMLEPNALDGRKAYFYQDLSFKKILAFPKTILLENDTIYH--DNPFIFRYDLNE 358
QY 361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 393
DB 359 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 418


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QY 394 -----DILRVNYDDLRVNYERLLQNASPLLELSQNTSFKTYRKAYOKPI 437
DB 419 YDILRVNCDILRVNYDDLRVNYERLLQNASPLLELSQNTTFKTYRKAYOKSL 470

RESULT 10
ADJ277810
ID ADJ277810 standard; protein; 486 AA.
XX
AC ADJ277810;
XX
DT 06-MAY-2004. (first entry)
XX
DE Helicobacter pylori strain 1182 FucB protein Segid 2.
XX
KM FucA; FucB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX
OS Helicobacter pylori.
XX
PN MO2004009838-A2.
XX
PD 29-JAN-2004.
XX
PF 23-JUL-2003; 2003WO-US023057.
XX
PR 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Johnson KF, Bezila DJ;
XX
DR WPI; 2004-123401/12.
DR N-PSDB; ADJ277809.
XX
PT New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
PT unglycosylated in its native form or for synthesizing glycolipids.
XX
XX Claim 16; SEQ ID NO 2; 72pp; English.
XX
CC This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (FucA and FucB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesize glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar, as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 1182 FucB protein sequence of the invention.
XX
SQ Sequence 486 AA;

Query Match 85.3%; Score 2036; DB 8; Length 486;
Best Local Similarity 81.2%; Pred. No. 3,8e-170;
Matches 384; Conservative 23; Mismatches 28; Indels 38; Gaps 2;

QY 1 MFQPLLDVAVESASIEKMAKSKPPKIVANWMBEIEKPKSVLYPIFSQRTYTLAH 60
DB 1 MFQPLLDVAITESASIEKITSKPPKIVANWMBEIEKPKSVLYPIFSQRTYTLAH 60
QY 61 QNPNFSDIVFSPNPGASARKIISYQNAKVFYTGENSEVNFNLFDAIGDFDELDFDRYL 120
DB 61 QNPNFSDIVFSPNPGASARKIISYQNAKVFYTGENSEVNFNLFDAIGDFDELDFDRYL 120
QY 121 RMPLYYDRLHHAESVNDTTSFYKLDKNSLYTLKKCSHQFKENHPNLCVAVNDESDPLKR 180
DB 121 RMPLYYDRLHHAESVNDTTSFYKLDKNSLYTLKKCSHQFKENHPNLCVAVNDESDPLKR 180
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DB 121 RMPLYYDRLHHAESVNDTTSFYKLDKNSLYTLKKPSHHFKENHPNLCVAVNDESDPLKR 180
QY 181 GYVSFVASNANPAPNAPFDALANSTIEPYVGGGSVKNTLIGVNVKNSSEPLSQYENL CFEN 240
DB 181 GPASFVASNPAPKNAFAFDVINSIEPVIGGSVKNTLIGNINKSEPLSQYFNLCFEN 240
QY 241 SOGQYVTEKILDAVESHTIPIYMGSPSVAKDQNPKEFVNVHDFNNFDEAIDYIKYLTHT 300
DB 241 SOGQYVTEKILDAVESHTIPIYMGSPSVAKDQNPKEFVNVHDFNNFDEAIDYIKYLTHT 300
QY 301 PNAVYDMLYENPLMALDGKAYFYODLSFKKILAEFFKTIENDTIYKSSSTSPMECDLDE 360
DB 301 PNAVYDMLYENPLMALDGKAYFYQNLSPFKKILDFPKTIENDTIYH--DNPFIFYEDLNE 358
QY 361 PLASL-----DILRVNYDDLRVNYDRLRV 384
DB 359 PLTISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRLV 418
QY 385 NYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNTSFKTYRKAYOKPI 437
DB 419 NYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKTYRKAYOKSL 471

RESULT 11
ADJ27345
ID ADJ27345 standard; protein; 486 AA.
XX
AC ADJ27345;
XX
DT 20-MAY-2004 (first entry)
XX
DE Alpha-1,3/4-fucosyltransferase.
XX
KM alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
KW fucosyl; fucose.
XX
OS Helicobacter pylori; strain 1182 FucB.
XX
PN MO2004009793-A2.
XX
PD 29-JAN-2004.
XX
PF 23-JUL-2003; 2003WO-US023155.
XX
PR 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Johnson KF, Bezila DJ;
XX
DR WPI; 2004-132958/13.
DR N-PSDB; ADJ27344.
XX
PT Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX
XX Claim 1; Fig 1; 84pp; English.
XX
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX
SQ Sequence 486 AA;

Query Match 85.3%; Score 2036; DB 8; Length 486;
```


DR WPI; 2002-582480/62.

PT	Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT	polypeptide useful for producing fucosylated oligosaccharides.

PS Claim 6; Fig 6; 37pp; English.

The invention relates a purified transmembrane segment-free alpha 1,3-fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is Ile, Val or Ala. Also included are the nucleic acid encoding the protein (including its complement or fragment), a vector containing the nucleic acid, a host cell containing nucleic acid or vector, an antibody which selectively binds to the protein and a gene expression system for producing transmembrane segment-free alpha1,3-fucosyltransferase, comprising a host cell modified with the nucleic acid or its enzymatically active portion. The protein and cells are useful for producing fucosylated oligosaccharides, such as lex, Ley or slex, by contacting the protein with a substrate, such as lactoNacR and GDP-fucose, and purifying the produced oligosaccharides, or by culturing the cell, contacting the host cell with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alpha1,3-fucosyltransferase polynucleotide, and detecting hybridisation of the probe; or by amplifying the nucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alpha1,3-fucosyltransferase-fusion protein, by growing the host cell containing a vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein and isolating the fusion protein. The antibody is useful for detecting the protein in a sample. The presence of the protein in the sample is indicative of infection by *Helicobacter pylori* or the presence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alpha1,3-fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alpha1,3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alpha1,3 fucosyltransferase encoded by the fuctr gene. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 485 AA;

Query Match	84.8%;	Score 2025;	DB 5;	Length 485;
Best Local Similarity	81.2%;	Pred. No. 2.9e-169;		
Best 384; Conservative	23;	Mismatches 28;	Indels 38;	Gaps 3;

Qy	1	MFQPLIDAYVEASASTIEMKASRSPPLKILIVAMWGBDEIKEFKKSUYLPIGQRYTIAH	60
Db	1	MFQPLIDAYIBESASIEKIRTSKSPPLUKLIVAMWGBEEVEEFKNILLYPLISQHYITTH	60
Qy	61	QNPNEPSDLVPSNPISGARKILISYONAKRVPYLYGENEVENPNFLFDAIGDELDPRDYL	120
Db	61	QNPNEPSDLVPSNPISGARKILISYONAKRVFYIGENESPFPNLFDAIGFDELDPRDYL	120
Qy	121	RMPLYYDRLHHAESVNDFTTSPYKLKDNLTYTLKKDSHOFKEMHPMLCAVNDSDPLKR	180
Db	121	RMPLYYDRLHHAESVNDFTTSPYKLKPDSTYALCKSSHFKENHPMLCAVANNESDPLKR	180
Qy	181	GVVSEFVASANANA PMRNAFYDALNSIEBPVYGGGSVKNTLGVYNNKSKSEFLSYKFNLCFEN	240
Db	181	GPASFPVANSNPNAPKRNAPFDVLNLSIEBPVYGGGSVKNTLIGNINIKSKSEFLSYQYFNLCFEN	240
Qy	241	SGGYGVTEKILIDAYFSHTTIPYWGSPSYAKDFNPKEFPVNVHD FNNPDEAIDYIKYLAFTH	300
Db	241	SGGYGVTEKILIDAYFSHTTIPYWGSPSYAQNDEPNKSPFNVCDFKDFEADIDVRYLAFTH	300
Qy	301	PNAVYIDMLYENPLNMDGKAYPQDLSFPKKILAFPTTILANDITTYHKSISFPMWECDDLE	360
Db	301	PNAVYIDMLYENPLNTLDGKAYFPQNLSPFKKILDFPTTILANDITTYH -DNMFLFYDNLN	358

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QY      361 PLAST-----DDLRVNYDDLRNV-----YDDLRV 384
Db      359 PLTIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 418
QY      385 NYDDLRVNYDDLRVNYDDLRVNYEELLONASPLELELSONTSFKLYRAYOXPI 437
Db      419 NYDDLRVNYDDLRVNYDDLRVNYEELLONASPLELELSONTSFKLYRAYOXSL 471

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RESULT 14
ADJ77820
ID ADJ77820 standard; protein; 425 AA.

AC	ADJ77820;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Helicobacter pylori strain 26695 PutA protein SegID 12.

FutA, alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; KW
FutB, alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; KW
fucose, N-acetylglucosamine; glycoconjugate; enzyme. KW

OS Helicobacter pylori.

PN WO2004009838-A2.

PD 29-JAN-2004.

PF 23-JUL-2003; 2003WO-US023057.

PR	23-JUL-2002; 2002US-0398156P
PR	08-NOV-2002; 2002US-0424894P

PA (NEOS-) NEOS TECHNOLOGIES INC.

PI Johnson KF, Bezila DJ;

DR WPI; 2004-123401/12.

[illegible]

new tobacco for
PT synthesizing

PT unglycosylated in its native form or for synthesizing glycolipids.

PS Claim 12; SEQ ID NO 12; 72pp; English..

This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (PutA and PutB) of *Helicobacter pylori* (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesize glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialylation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 26695 PutA protein sequence of the invention.

SQ Sequence 425 AA;

	Score	DB	Length
Query Match	82.6%	8	425
Best Local Similarity	85.8%		
Matches 376; Conservative		126-164	
		9; Mismatches	29; Gaps

QY 1 MFQPLLDAYVESASIEKAKSK-PPPLKIAVANWMDDEEIKKKSVLPITBSORIAL 59
:
Db 1 MFQPLLDAYVESASIEKAKSKPPPLKIAVANWMDDEEIKKKSVLPITBSORIAL 60
QY 60 HONPNEFSDLYVSNPLGSAARKILSYONAKRVPTGTENEVENFLPYAIGDFDEIDPDRY 115
:
Db 61 HONPNEFSDLYVSNPLGSAARKILSYONAKRVPTGTENEVENFLPYAIGDFDEIDPDRY 120

```
QY 120 LRMPLYYDLHFKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNHPNLCAVNDSDPLK 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LRMPLYYALHFKAEVNDTTAPYKDKNSLYALKKPSHHFKKNHPNLCAVNDSDPLK 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 RGVVSFVASNANAPMNAFYDALNSIEPVYGGSVKNTLGYVKNKSEFLSQYKFNLCFE 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 RGFASFVASNANAPMNAFYDALNSIEPVYGGSVKNTLGYVKNKSEFLSQYKFNLCFE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 NSQGYGVYTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLT 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 NSQGYGVYTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLT 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 HNNAYIDMLYENPILNLDGKAYFYODLSFKKILAFPKTILENDTIYHKSSTSPWMECDLD 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 HNNAYIDMLYENPILNLDGKAYFYODLSFKKILAFPKTILENDTIYHKSSTSPWMEYDLH 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 EPLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLE 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 KPLVGSIDDLRVNYDDLRVNYD-----RLDQNASPLLE 392
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 LSQNTSFKTYRKAYQKPI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 LSQNTTFKTYRKAYQKSL 410
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ADJ27355
ID ADJ27355 standard; protein; 425 AA.
AC ADJ27355;
DT 20-MAY-2004 (first entry)
DB Alpha-1,3/4-fucosyltransferase.
KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
  fucosyl; fucose.
XX Helicobacter pylori; strain 26695FutA.
XX WO2004009793-A2.
XX 29-JAN-2004.
XX 23-JUL-2003; 2003WO-US023155.
XX 23-JUL-2002; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
XX (NEOS-) NBOSE TECHNOLOGIES INC.
XX Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX N-PSDB; ADJ27354.
XX Producing fucosylated glycoprotein, by contacting recombinant
  PT fucosyltransferase protein with mixture comprising donor substrate and
  PT acceptor substrate on glycoprotein.
XX Example 1; Fig 6; 84pp; English.
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which
  CC was used in the method of the invention for producing a fucosylated
  CC glycoprotein. The method involves contacting a recombinant
  CC fucosyltransferase protein with a mixture comprising a donor substrate
  CC which comprises a fucosyl residue, and an acceptor substrate on a
  CC glycoprotein, under conditions such that the fucosyltransferase protein
  CC catalyzes the transfer of the fucose residue from a donor substrate to
  CC the acceptor substrate on the glycoprotein. The method is useful for
  CC producing fucosylated glycoprotein.
XX
```

```
SQ Sequence 425 AA;
Query Match 82.6%; Score 1972.5; DB 8; Length 425;
Best Local Similarity 85.8%; Pred. No. 1.2e-164;
Matches 376; Conservative 9; Mismatches 24; Indels 29; Gaps 2;

QY 1 MFQPLDAAVESASIEKNASKS-PPPLKIAVANNMGDEIEKFKSVLYIFPSQRYTAL 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFQPLDAAVESASIEKNASKSPPPLKIAVANNMGDEIEKFKSVLYIFPSQRYTAL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 HNNERSDLYFSNPLGARKILSYQNAKRVFYTGSENVNPNLPDYAIGPELDFRDY 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 HNNERSDLYFSNPLGARKILSYQNTKRVFYTGSENVNPNLPDYAIGPELDFNDY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 LRMPLYYDLHFKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNHPNLCAVNDSDPLK 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LRMPLYYALHFKAEVNDTTAPYKDKNSLYALKKPSHHFKKNHPNLCAVNDSDPLK 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 RGVVSFVASNANAPMNAFYDALNSIEPVYGGSVKNTLGYVKNKSEFLSQYKFNLCFE 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 RGFASFVASNANAPMNAFYDALNSIEPVYGGSVKNTLGYVKNKSEFLSQYKFNLCFE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 NSQGYGVYTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLT 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 NSQGYGVYTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLT 300
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QY 300 HNNAYIDMLYENPILNLDGKAYFYODLSFKKILAFPKTILENDTIYHKSSTSPWMECDLD 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 HNNAYIDMLYENPILNLDGKAYFYODLSFKKILAFPKTILENDTIYHKSSTSPWMEYDLH 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 EPLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLE 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 KPLVGSIDDLRVNYDDLRVNYD-----RLDQNASPLLE 392
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 LSQNTSFKTYRKAYQKPI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 LSQNTTFKTYRKAYQKSL 410
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: August 11, 2006, 19:36:48
Job time : 118.648 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:37:09 ; Search time 20.9374 Seconds
(without alignments)
2049.570 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 2388
Sequence: 1 MFQPLDVAYESASIEKMAS.....KIYKAYQKPIKNPYCAP 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2058.5	86.2	476	2 C64601	fucosyltransferase
2	1972.5	82.6	425	2 C64567	fucosyltransferase
3	1959.5	82.1	454	2 B71914	alpha (1,3)-fucosyl
4	1917	80.3	436	2 G71862	alpha-(1,3)-fucosyl
5	193	8.1	346	2 T44327	hypothetical prote
6	160.5	6.7	2657	2 T18497	hypothetical prote
7	149.5	6.3	513	2 P96533	hypothetical prote
8	144	6.0	525	2 T28306	ORF MSV145 hypothe
9	142.5	6.0	789	2 G90587	lipoprotein (impor
10	142.5	6.0	2708	2 T09079	probable chloroqui
11	141.5	5.9	183	2 C97832	alpha-(1,3)-fucosyl
12	141.5	5.9	433	2 A57596	alpha-1,3-fucosyl
13	139.5	5.8	1532	2 T18438	hypothetical prote
14	135	5.7	2819	2 T09080	probable chloroqui
15	134.5	5.6	747	2 H82943	hypothetical prote
16	133	5.6	790	2 T50337	homolog to drosoph
17	133	5.6	5005	2 P82884	hypothetical prote
18	132.5	5.5	1272	2 H82926	conserved hypotet
19	129.5	5.4	393	2 H96742	hypothetical prote
20	128.5	5.4	400	2 JC4591	alpha-1,3 fucosyl
21	128	5.4	653	2 B81277	hypothetical prote
22	127.5	5.3	498	2 D71616	ribosome releasing
23	125.5	5.3	365	2 S55498	alpha (1,3/4)-fucos
24	125.5	5.3	451	2 T23491	hypothetical prote
25	125.5	5.3	1138	2 A82939	membrane nuclease
26	125	5.2	737	2 C70132	hypothetical prote
27	124.5	5.2	2500	2 G71609	hypothetical prote
28	124	5.2	563	2 B82883	hypothetical prote
29	123.5	5.2	1061	2 D98008	conserved hypotet

30	123	5.2	405	2 B36340	alpha (1,3)-fucosyl
31	123	5.2	1712	2 C71618	hypothetical prote
32	121.5	5.1	2269	2 T18472	hypothetical prote
33	121	5.1	1181	2 B64516	hypothetical prote
34	121	5.1	1291	2 T40631	non-proteolytic bo
35	119	5.0	359	2 A45156	alpha-(1,3)-fucosyl
36	119	5.0	960	2 S72284	DNA-directed RNA p
37	118.5	5.0	1127	2 T28317	ORF MSV156 hypothe
38	118.5	5.0	1306	2 G90085	ORF MSV152 probabl
39	118.5	5.0	2339	2 A45597	DNA-directed RNA p
40	118.5	5.0	2380	2 B71604	hypothetical prote
41	118	4.9	364	2 I39048	alpha (1,3) fucosyl
42	117.5	4.9	532	2 G30085	hypothetical prote
43	117	4.9	324	2 A11879	hypothetical prote
44	116	4.9	361	2 A36659	3-alpha-galactosyl
45	116	4.9	1132	2 H82887	hypothetical prote

ALIGNMENTS

RESULT 1					
Fucosyltransferase - Helicobacter pylori (strain 26695)					
C:Species: Helicobacter pylori					
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004					
C:Accession: C64601					
R:Tomb, J.F.; White, O.; Kierlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997					
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.N. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A:Reference number: A64520; MUID:97394467; PMID:9252185					
A:Accession: C64601					
A:Status: preliminary; nucleic acid sequence not shown; translation not shown					
A:Molecule type: DNA					
A:Residues: 1-476 <TOM>					
A:Cross-References: UNIPROT:O23366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID:					
Query Match 86.2%; Score 2058.5; DB 2; Length 476;					
Best Local Similarity 84.5%; Pred. No. 8.5e-130;					
Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;					
QY	1	MFQPLDVAYESASIEKMASKS-PPPLKIAVAMWGDBEIKFKSVLYTFISQRTTAL	59		
DB	1	MFQPLDVAIESASIEKMASKSPPPLKIAVAMWGDBEIKFKSVLYTFISQRTTAL	60		
QY	60	HONNEESDLVFSNPLGSAKILSYONAKGVFTGENEVPENLFDVAIGDELDPRRY	119		
DB	61	HONNEESDLVFSNPLGSAKILSYONAKGVFTGENEVPENLFDVAIGDELDPRRY	120		
QY	120	LRMPLYYDRLHKKASVNDTTSPYKLDKNSLYTLKKSHQKKNHPMLCAVNDSDPLK	179		
DB	121	LRMPLYYAHLYRELVNDTTPYKLDKNSLYTLKKSHQKKNHPMLCAVNDSDPLK	180		
QY	180	RGVVSFYASNANAPRNAPFDALNSIEPVYGGGVKNTLGVYKXKSEFISQYFNLCFE	239		
DB	181	RGFASFYASNANAPRNAPFDALNSIEPVYGGGVKNTLGVYKXKSEFISQYFNLCFE	240		
QY	240	NSQGYGVTEKILDAVYSHITPIYMGSPSAKOPNPEFVNVVHDPNNFDEAIDYIKYIHT	299		
DB	241	NSQGYGVTEKILDAVYSHITPIYMGSPSAKOPNPEFVNVVHDPNNFDEAIDYIKYIHT	300		
QY	300	HPNAVYLMYENPLNADGKAYFYODLSPFKKILAFPTIILENDITYKSSFSFMWCDLD	359		
DB	301	HPNAVYLMYENPLNADGKAYFYODLSPFKKILAFPTIILENDITYKSSFSFMWCDLD	360		
QY	360	EPLASI-----DILRVYDDLRVYDDLRVYDDLRVYDDLRV	391		
DB	359	EPLISIDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRV	418		
QY	392	NYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRV	437		

Db 419 NYDDLKRVYDDLKRVNYDKLONASPLLELSQNTTKTKTKAYOKSL 464

RESULT 2

fucosyltransferase - Helicobacter pylori (strain 26695)

C64567

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: C64567

R/Tomb, J.F.; White, O.; Kesteven, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khair, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: C64567

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-425 <TOM>

A/Cross-references: UNIPROT:025142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID

Query Match 82.6%; Score 1972.5; DB 2; Length 425;

Best Local Similarity 85.8%; Pred. No. 3,9e-124;

Matches 376; Conservative 9; Mismatches 24; Indels 29; Gaps 2;

1 MFQPLDVAVESASIEKMAKSKS-PPPLKIAVANMMGDEBEIKPKSVLYFISQRYTIAL 59

1 MFQPLDVAFIESASIEKMAKSKSPPLKIAVANMMGDEBEIKPKSVLYFISQRYAIDL 60

60 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGSENVFNPLPDYALGFDELDFRDR 119

61 HONPNEFSDLVFNSPLGSAKILSYONTKRVYTGSENVFNPLPDYALGFDELDFRDR 120

120 LRMPLYYRLHKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNPNLCAYVNDESDPL 179

121 LRMPLYYRLHKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNPNLCAYVNDESDPL 180

180 RGVNSFVANSNANAPRNAPFYDALNSIEPVYGGGVKNTLGYVVKKSEFLSQYKFNLCF 239

181 RGVNSFVANSNANAPRNAPFYDALNSIEPVYGGGVKNTLGYVVKKSEFLSQYKFNLCF 240

240 NSQGYGYTEKILDAVFSHTTPIYWGSPSVADFPNKEFVNVDENNDEALDIYIKYLT 299

241 NSQGYGYTEKILDAVFSHTTPIYWGSPSVADFPNKEFVNVDENNDEALDIYIKYLT 300

300 HPNAVYLDMLYENPLNALDGKAYFYODLSFKTILAFPKTILENDTIYHKSTSPFMECDL 359

301 HPNAVYLDMLYENPLNALDGKAYFYODLSFKTILAFPKTILENDTIYHKSTSPFMECDL 360

360 EPLASIDDLRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDL 419

361 KPLVSIIDDLRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDL 420

420 LSQNTSPFKTKRKYOKPI 437

393 LSQNTSPFKTKRKYOKSL 410

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-454 <ARN>
A/Cross-references: UNIPROT:Q9ZL13; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NID:
A/Experimental source: strain J99
C/Genetics:
A/Gene: fuct

Query Match 82.1%; Score 1959.5; DB 2; Length 454;

Best Local Similarity 83.2%; Pred. No. 3.2e-123;

Matches 371; Conservative 25; Mismatches 37; Indels 13; Gaps 4;

1 MFQPLDVAVESASIEKMAKSKSPPLKIAVANMM--GDEBEIKPKSVLYFISQRYTIA 58

1 MFQPLDVAFTSDTRDETYK--PPLNKIAVANMMPLDKESKGRFRFLYFISQRYTIT 58

58 LHONPNEFSDLVFNSPLGSAKILSYONAKRVYTGSENVFNPLPDYALGFDELDFRDR 118

59 LHONPNEFSDLVFNSPLGSAKILSYONTKRVYTGSENVFNPLPDYALGFDELDFRDR 118

119 YLRMPLYYRLHKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNPNLCAYVNDESDPL 178

119 YLRMPLYYRLHKAESVNDTTSPTKDKNSLYTLKKPSHOFKKNPNLCAYVNDESDPL 178

179 RGVNSFVANSNANAPRNAPFYDALNSIEPVYGGGVKNTLGYVVKKSEFLSQYKFNLCF 238

179 RGVNSFVANSNANAPRNAPFYDALNSIEPVYGGGVKNTLGYVVKKSEFLSQYKFNLCF 238

239 ENSQGYGYTEKILDAVFSHTTPIYWGSPSVADFPNKEFVNVDENNDEALDIYIKYLT 298

239 ENSQGYGYTEKILDAVFSHTTPIYWGSPSVADFPNKEFVNVDENNDEALDIYIKYLT 298

299 THPNAYLDMLYENPLNALDGKAYFYODLSFKTILAFPKTILENDTIYHKSTSPFMECDL 358

299 THPNAYLDMLYENPLNALDGKAYFYODLSFKTILAFPKTILENDTIYHKSTSPFMECDL 358

359 DEPLASIDDLRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDL 411

359 DEPLASIDDLRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDLKRVNYDDL 411

412 QNASPLLELSQNTTKTKTKAYOKPI 437

417 QNASPLLELSQNTTKTKTKAYOKSL 442

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

A:Gene: F14J22.8
A:Map position: 1

Query Match
Best Local Similarity 22.2%; Pred. No. 0.017;
Matches 53; Conservative 40; Mismatches 79; Indels 67; Gaps 8;

Qy 172 NDESDPLKRG--VVSFVSNANAPMEN--AFYDALNSIEPYTG----- 210
Db 177 NDLAQARRRGYDVTWTTSSSDVPVGYFSMAEYDIMSPOQPTKERALAAAFISNCGRNF 236

Qy 211 -----GGSVKNTLGYNVKKSSEFLSQYKFNLCFENSOGGYVTEKTL 252
Db 237 RLQALEALMKTNIKIDSYGGCHNRDG--KVDKVBALKRYKFSLAPEMNEEDYVTEKFF 294

Qy 253 DAYESHTPIYWGSPSVAKDFNP--KEFVNVDHFNNDFAIDYIKYLAHTHPNAYLDML-- 308
Db 295 QSLVAGSPVAVVGPNNI--BEFAPASDSFLHITKTMEDVEVPAKRMKYLAAFPAYNQTLFW 353

Qy 309 -YENPLNALDGKAYFYQDLSFKKILAFKTYIE-----NDTIYH 346
Db 354 KYEGSDSDFKALVDMAAAVHSSCRCTI FLATRVREQEESPNFKQPCCKSGSGSDTVYH 412

RESULT 8
T28306
ORF MSV45 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #ext_change 09-Jul-2004
C:Accession: T28306
R:Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J: Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Accession: T28306
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-525 <AFO>
A:Cross-references: UNIPROT:Q9YVU7, UNIPARC:UP100000F556B; EMBL:AF063866; NID:ig4049647;
C:Genetics:

Query Match
Best Local Similarity 19.3%; Pred. No. 0.04;
Matches 107; Conservative 76; Mismatches 176; Indels 194; Gaps 29;

Qy 1 MEQPLDAAVESASIEKMAKSPPLKIVANMMGDEBEKEFKSYLPIFSQRYTIALH 60
Db 14 LYTPTMNNLIEKYGIDKIPN-----NVCITN-----NSYFYILLIEMONYDIY 56

Qy 61 QNPNEFSDLVFNPLGSARKILSYQNAKRVFYTGNEVPNF-----NLFPYALIGDELDER 116
Db 57 DKISKYKILIHNL--RQIMNSTDLKEYT-----NNIINIDNYKSLSYIIN-----KFW 105

Qy 117 DRYLWMP-----LYYDLHAKASVNDT-----SPYKAD 147
Db 106 DKYVNVPPSININIDNIKINIVSSLSKVVYTKYYD-----PNKVTBELLFTYYSKD 157

Qy 148 NSLYTLKESHPKKNHPLCAVNDSDPLKRGVSPVASNANAPRANAFAALNSIEP 207
Db 158 LAISILYNDAAIDITFDMLLETIND-----RSIPSYINTN-----YYLFPKS-- 201

Qy 208 VTGGGSVKNTLGYNVKKSSEFLSQ--YKFNLCFENSOGGYVTEKILDAVFS----- 257
Db 202 -----SLK-TIEYKFKVSSNDPGLMKSRSEFELKNDGY-AKQPNVDVFISILYSYR 254

Qy 258 -----HTPIY--WGPSVAKDFNP-----KEFVNVDHFN 286
Db 255 NGFVTHNIIITWYTLFGYKILRODLKELPAIKNIPLELSGISDLLINQNTYAIDEILN 314

Qy 287 FDEALDIYKYLHHPAYLDMLENPPLNALDG-----KAYFYQ-DLSFKIL--LAF 334
Db 315 HDE--PKITIEIGQIVNTSENVNNTYINVLIESIAKKPFEKGYFYNFDVINKLKFNKFF 372

Qy 335 EKTILENDTI-----YKSSSTFMWEGCDLDEPLASIDDLRVNYDDLRVYDD 381
Db 373 FNFLEYYNPIISDIDILNKKIELANKN-----EGGLD-----YID---KTKLYNTYML 419

Qy 382 LRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELS--QNTSFKI----- 428
Db 420 INNNTSDFENVLY-----NYEYVFKPENNMYDIIEDLFELSIISKLKILFERYSFIPKN 474

Qy 429 ---YRKAYQKPIK 438
Db 475 ITNLRQYWEHIK 487

RESULT 9
G90587
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 09-Jul-2004
C:Accession: G90587
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mozer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; NUID:21267165; PMID:11353084
A:Accession: G90587
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-789 <KUR>
A:Cross-references: UNIPROT:Q9PW2, UNIPARC:UP100000C80CE; GB:AL445566; PID:g14090022; P1
C:Genetics:
A:Experimental source: strain UAB CTIP
A:gene: MTPU 6070
A:genetic code: SGC3

Query Match
Best Local Similarity 21.4%; Pred. No. 0.087;
Matches 107; Conservative 76; Mismatches 174; Indels 143; Gaps 27;

Qy 51 FSGRYTIALHONPEFSDLVFNPLGSARKILSYQNAKRVFYTGNEVPNFNI-----FDY 106
Db 136 YDSKVILTSSENPSSINSKDFKNLKKAKIEVFLKEKN-YLNNEKLSYSISKAMDFFY 194

Qy 107 AIGFDEL-DPRDRY-LRMLPYDRLHAKASVNDTTSPTYLKONSU-----YTLKKPSHQ 159
Db 195 SLMRDLSLSIRKDMNISLKNNEINRK-WNLKNKLSLYKINDEDLFDKNNYNDQNSIT 253

Qy 160 F-KENHPLCAVNDSDPLKRGVSPVASNANAPRANAIFYDALNSIEPYTGGSVNTL 218
Db 254 FNKNQMDRAGFEENEL-----IQNLVFSPVSSDPIHDTFDALN-----YGLQSYGKTL 302

Qy 219 GYNNKKSSEFLSQYKFNLCFENSOGGYVTEKILDAVFSHTPIYWGSP-----SVAKD 272
Db 303 -----NDSLFLSDYVF--ISNT-----IEKQFIDNSDLDVLYNKPRLRVHINVTISP 349

Qy 273 FNPKEFVNVDHFN-----NPEKADIVYK-----Y 296
Db 350 LNKQAY-KIQSFNRFNKNSLSTLDVDSLMLSDANDVIKQORYKI SYNSLNSNNINIKIP 408

Qy 297 LHTHPNAYLDMLENPPLNALDGKA--YFYQDSFPK----- 329
Db 409 WKLIPESTSNFENENKGLIYGDLNANFYFNDSFEFRNNLSMLINYPALNFSKKTWY 466

Qy 330 -----KILAFKTYILEN-----DTIYKKS--TSFMECDLDEPLASIDDLRVNY-- 372
Db 469 HSYANNNMLFGKQNGQNNVNNKLYDAYYHLNSFTSFKKESINE--NIIQSEKFFLYFK 525

Qy 373 DDLR-----VNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQN--TSF 426
Db 526 DDQNNILKSNRPFKIKKNLNLHLDNF-----INQNNIKGNBEMQI-----PYEKAINQEKY 577

Qy 427 KIYRKAYQKPIKPNPYCAP 446
Db 578 FAYNOYIQL-IKSIHPSLKP 596

C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18438
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: T18935
A:Accession: T18438
A:Status: preliminary; translated from GB/EMBL/DBD
A:Residues: 1-1532 <L9>
A:Molecule type: DNA
A:Cross-references: UNIPROT:O77332; UNIPARC:UPI0000017CC26; EMBL:Z98547; NID:e1325376; P
C:Genetics:
A:Map position: 3
A:Note: C0415C

Query Match 5.8%; Score 139.5; DB 2; Length 1532;
Best Local Similarity 21.0%; Pred. No. 0.34;
Matches 89; Conservative 59; Mismatches 147; Indels 129; Gaps 19;

48 YEIFSGRYTIALHQ-NPEPSDLVSNPLSGARKILSYONAKRVYTGEEVNPENLFDY 106
457 YNSFLQKYLILYKLMERFIKIL-----KKILS-----KLFYPLQNKSLIN----- 500
107 ALGFDEL-----DPRD-----RYLRLPLYYDRLLHKKASVNDTTSPLYL 145
501 --GFDLILKSLIKIILINGSFNDIMITYRWROYIFYKTYNKKOREKEKSI----- 549
146 KNSLTLYLKKPSHQFK-NHNPILCAVNVESDP-----LKGVSFVA----- 187
550 KSNNTY-----NMIFDMNENL---INFETDPHFVYNDIQKIIQMLCHETIQENKD 601
188 ----SNANAPMRAVPAFDALNSIEPVGGGVKNTLYGVYKN-----KSEPLSYKPNLC 237
602 NTKYDPTNNEVYNTFYS--NHMHNHNSSYLQNNNIFHLSDLILYMKKDYIKIYEF-LT 658
238 FENSQGYVTEKILDAYFSHTIPIYWGSPV-----ADPNPKFVNVH 282
659 FTIIEKQQTNTLMFDKYPFKSMITIMINKQIKLFCVEINRKYVYSIESGDTKMLFECAV 718
283 DFNPNDEALDIYIKYLHTHPNAYLDMLEYENPNALDGKAYFYODLSFKKILAFPTILEND 342
719 NFNNDPV-----YHHT-----SQLNHGKEMKEQFLGKKKINNIGIRKIDED 762
343 IYHKSTSEFMWECDDLEPLASIDDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDD 402
763 DLY-----CNEDDIYCNEDDIYCNEDDIYCNEDDIYCNEDDIYCNEDDIYCNEDD 812
403 LRVN 406
813 TYCN 816

RESULT 14
T09080
Probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T09080
R:Su, X.Z.; Kirkman, L.A.; Fujioaka, H.; Wellens, T.E.
Cell 91, 593-603, 1997
A:Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A:Reference number: Z16556; MUID:98054002; PMID:9393853
A:Accession: T09080
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-2819 <SUX>
A:Cross-references: UNIPROT:O15792; UNIPARC:UPI00000785E5; EMBL:AF030693; NID:g2642515;
A:Experimental source: strain HB3; from Honduras
C:Genetics:
A:Gene: CG2
C:Keywords: toxin resistance

Query Match 5.7%; Score 135; DB 2; Length 2819;

Best Local Similarity 20.1%; Pred. No.1.5; Mismatches 89; Conservative 72; Mismatches 140; Indels 142; Gaps 22;

Query 42 PKKSVLYFISQRYTIA-----LHQNPBFSDLVFSNPISGARKILSYONAKRVFTTGEN 96
Db 1887 FLPLVLYVNFVFFRLTGLVWLTLLGLTKNDYTDINLRDENC-NVQYITLAKNSKSWD 1945
QY 97 ----EVPNPLFDYALGDELDFRDRYLRLMPLRYDLRHKASVNDTSPYKLKDN----- 148
Db 1946 QPNPEVKNMT-----DE-----NNTYTTKKKQDNDNQ 1974
QY 149 -----SLYT-----LKKSHQFKNHNPILCAVNDSDPLKRGVVS 184
Db 1975 NDDIYIHLINNIYVNTIYTERLINDRKISNAKKETETHTMTDILFNDNNCIN---II 2031
QY 185 FVASNANAPMENAFYDAL--NSIEPVTG--GGSVNTLGYVNVKKSBEFLSOYKFNLCFE 239
Db 2032 NVEDNKENINIDLKKYKKTMEVEKVDNBEFQVTDNNIILINPKKSTISONEQHINNTI 2091
QY 240 NSQGYIYTEKILDAYFHSHTPI-YWGSBSVAKDRPKFVNVHDNNDEALDIYKYLH 298
Db 2092 NENGMYTYSILNSTLTJLNNHMKW-----KYLINTYCFNN-----YIMFQ 2134
QY 299 THPAVYLDMLLENPLN-ALDGKAYFYODL--SPKKILAFPTILE-----NDTIYHKS 349
Db 2135 TTQNKYL-----LNRRLIKAFPLRSIKFDFDNDIKSYKKVKEINICDNNHKKMD 2187
QY 350 TS-----FMWECDDLEPLASIDDLRVN--DDLRVN-----YDDLRVNVD-- 388
Db 2188 TAQGYIHLKDKQKKEKELINFDHI-INTWSDMIWVSQIHVLTGHSISLYENVEEVD 2246
QY 389 -----LRVNVDDLVRVND 402
Db 2247 AMFYCLQKKKKGNDNNKNGDN 2269

RESULT 15
H82943
hypochemical protein UN030 [imported] - ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #ext_change 20-Aug-2000
C:Accession: H82943
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A:Reference number: A82870
A:Accession: H82943
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-747 <GLA>
A:Cross-references: UNIPARC:UPI00013913A; GB:AE002102; GB:AF222894; NID:G6898967; PIDN:;
A:Experimental source: serovar 3, biovar 1
C:Genetics:
A:Gene: UN030
A:Genetic code: GCG3

Query Match 5.6%; Score 134.5; DB 2; Length 747;
Best Local Similarity 20.7%; Pred. No. 0.28;
Matches 99; Conservative 77; Mismatches 163; Indels 139; Gaps 26;

QY 16 EKMAKSPPEPLKIAVANWKGDE-----IKERKKSVLTYIFSQRYTIALHQNPNEF 66
Db 89 EKILDKN-----DYELIIMWANDNDGTLAGINITYIKTKQS--YLIINPKPVLTDKQN-NYL 141
QY 67 SDLVESNP-IGSARKILSYQN-----AKGVFYGENEVPNPLFDYA 107
Db 142 QELKTKTPAVYSIDELTKSNPNYLIHNPPYRQELAPKITYFNQNEAVNDSDKLYMKN 201
QY 108 IGFDELD-----FDRYLRMPLY-YDRLHRAESVNDTSPYKLKONSLYTLK-- 154
Db 202 IGYSEFGSDVQKRLKNAFKIRYDEQNIYQINSQIILAKETKLTYSIDKTKNNNYSINIE 261
QY 155 -----KPSHQFKNHNPILCAVNDSDPLKRGVVSFVASNANAPMENAFY----DALN 203

Db 262 LKGLIQNPFGKLPKFAQLINLIKKEYP-KELTTKNESVDNIYVKDIYRIIDRYA 320
QY 204 SIEPVVG--GGSVKNTL-----GYNVK-----KSEFLSOYKENLCF-----EN 240
Db 321 KLEFIEIYNKTKYQYVYLSANFNQKNSGLKKNEDYFQYLPDRTISLDLTTKDGKNVEL 380
QY 241 SOGYGVTEKILD-----AVFSHTIPIYMGSPSVAKD-----FNPKEFVNV 281
Db 381 NSGTGWIVDRITIDSLPKKIKILIAITNNHYMG--WSNLAI SKDNRMKSRWFNKQYINY 438
QY 282 HDEN-----NFDEALDYIKYLTHTHPNAYLDMLYENPLNALDGKAYFYODLSFKKILAF 335
Db 439 LENNAGFISSNIEYEDKORYQL-LMGTAPLKSPVSNKYNLSLG-----ISFENLA--- 487
QY 336 KTIENDTIYHKSSTSPM--WECDDLEPLASIDDLAVNTDDLAVNTDDLAVNTDDLAV 390
Db 488 -----KYNITNQNFINRAWYI---POLSANGIKIN-ENLRTWY---QINQEDIK 530

Search completed: August 11, 2006, 19:45:57
Job time : 22.9374 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:30:58 ; Search time 156.864 Seconds
(without alignments)
2630.023 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 2388

Sequence: 1 MFQPLLDAYVESASIERKMAS.....KIYRKAYQKPIKNPPYCAP 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred.-No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	87.1	478	2	O30511_HELPY
2	2058.5	86.2	476	2	O25366_HELPY
3	1972.5	82.6	425	2	O25142_HELPY
4	1959.5	82.1	454	2	O25142_HELPY
5	1917	80.3	436	2	O25142_HELPY
6	1894.5	79.3	432	2	O25142_HELPY
7	1812.5	75.9	462	2	O25142_HELPY
8	1502.5	62.9	333	2	O25142_HELPY
9	442.5	18.5	331	2	O25142_HELPY
10	419	17.5	359	2	O25142_HELPY
11	309	12.9	287	2	O25142_HELPY
12	193	8.1	346	2	O25142_HELPY
13	192.5	8.1	389	2	O25142_HELPY
14	191.5	8.0	462	2	O25142_HELPY
15	182	7.6	665	2	O25142_HELPY
16	177.5	7.4	444	2	O25142_HELPY
17	176	7.4	600	2	O25142_HELPY
18	175	7.3	417	2	O25142_HELPY
19	175	7.3	2359	2	O25142_HELPY
20	170.5	7.1	818	2	O25142_HELPY
21	166.5	7.0	348	2	O25142_HELPY
22	166	7.0	338	2	O25142_HELPY
23	164.5	6.9	533	2	O25142_HELPY
24	163.5	6.8	413	2	O25142_HELPY
25	163	6.8	338	2	O25142_HELPY
26	162.5	6.8	349	2	O25142_HELPY
27	162.5	6.8	463	2	O25142_HELPY
28	160.5	6.7	777	2	O25142_HELPY
29	160.5	6.7	2870	2	O25142_HELPY
30	159.5	6.7	510	2	O25142_HELPY
31	159.5	6.7	533	2	O25142_HELPY

32	158.5	6.6	359	1	FUT9_RAT	O99jb3 rattus norv
33	158.5	6.6	504	2	Q6Q5Y3_MEDTR	Q6Q5Y3 medicago tr
34	158.5	6.6	1330	2	O81BJ3_PLAF7	O81BJ3 plasmodium
35	158	6.6	465	2	O54PK3_DICDI	O54pk3 dictyosteli
36	156.5	6.6	505	2	O54PK3_MEDSA	O54pk3 medicago sa
37	156.5	6.6	506	2	O54PK3_MEDTR	O54pk3 medicago tr
38	155.5	6.5	219	2	Q93WS0_MEDTR	Q93ws0 medicago tr
39	155.5	6.5	359	1	FUT9_MOUSE	O8819 mus musculu
40	155.5	6.5	359	2	Q3TG63_MOUSE	O3tg63 mus musculu
41	155.5	6.5	385	2	O5F2P2_ORYLA	O5f2p2 oryzias lat
42	155.5	6.5	522	2	O599J4_9ROSI	O599j4 populus alb
43	155	6.5	349	2	Q3KQ28_XENLA	Q3kq28 xenopus lae
44	155	6.5	349	2	Q7SZU7_XENLA	Q7szu7 xenopus lae
45	155	6.5	471	2	Q6A1G3_XENTR	Q6a1g3 xenopus tro

ALIGNMENTS

RESULT 1				
O30511_HELPY				
ID	O30511_HELPY	PRELIMINARY;	PRT;	478 AA.
AC	O30511;			
DT	01-JAN-1998, integrated into UniProtKB/TrEMBL.			
DT	01-JAN-1998, sequence version 1.			
DT	07-FEB-2006, entry version 26.			
DE	Alpha1.3-fucosyltransferase.			
GN	Name=fuct;			
OS	Helicobacter pylori (Campylobacter pylori).			
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;			
OC	Helicobacteraceae; Helicobacter.			
OX	NCBI_TaxID=210;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=NCTC 11639;			
RX	MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;			
RA	Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.;			
RT	"Cloning and heterologous expression of an alpha1.3-fucosyltransferase gene from the gastric pathogen Helicobacter pylori.";			
RL	J. Biol. Chem. 272:21357-21363(1997).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; AF008596; AAB81031.1; --; Genomic_DNA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008417; P:fucosyltransferase activity; IEA.			
DR	GO; GO:0016757; P:transferase activity, transferring glycosyl. .; IEA.			
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.			
DR	InterPro; IPR001503; Glyco_trans_10.			
DR	PANTHER; PTHR11929; Glyco_trans_10.			
KW	Glycosyltransferase; Transferase.			
SQ	SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;			
Query Match				
Best Local Similarity 87.1%; Score 2079; DB 2; Length 478;				
Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;				
QY	1	MFQPLLDAYVESASIERKMASPPPLKIAVANWGDDEEIKPKSVLYIFISQRYTIALH	60	
Db	1	MFQPLLDAYVESASIERKMASPPPLKIAVANWGDDEEIKPKSVLYIFISQRYTIALH	60	
QY	61	QNPNEFSDLVFNPILGSAKILSYQNAKRVFTYGENEVFNFLFDVAIGFDELDFRDRL	120	
Db	61	QNPNEFSDLVFNPILGSAKILSYQNAKRVFTYGENEVFNFLFDVAIGFDELDFRDRL	120	
QY	121	RMPLYDRLHHAESVNDTTSYKLNKNSLYTLKPKSHQFKNHNLCAVNVNDESDPLK	180	
Db	121	RMPLYDRLHHAESVNDTTSYKLNKNSLYTLKPKSHQFKNHNLCAVNVNDESDPLK	180	
QY	181	GVVSFVSNANAPMNAFYDALNSLEPTVGSGSVKNTLGYNVNKNSEFLSQYKFNLCFEN	240	
Db	181	GVVSFVSNANAPMNAFYDALNSLEPTVGSGSVKNTLGYNVNKNSEFLSQYKFNLCFEN	240	

```
QY 241 SQGYVTEKILDAYFSHTTPIYWGSPSVAKDNFKPFVNVHDFNNFDEADYIKYLHTH 300
Db 241 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 TQGGYVTEKILDAYFSHTTPIYWGSPSVAKDNFKPSFNVHDFNFKFDEADYIKYLHTH 300
Db 301 PNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIYHKSSSTSFNWECDLDE 360
Db 301 KNAVLDMLYENPLNLTDGKAYFYQDLSFKKILAFPKTILENDTIYH--DNFFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 392
Db 359 PLVTIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 418
QY 393 YDDLVRVNYDDLVRVNYERLLQNASPLLELSQNTSPKIYRKAYOKPI 437
Db 419 YDDLVRVNYDDLVRVNYERLLSKATPLLELSQNTSTKIYRKAYOKSL 463

RESULT 2
O25366_HELPY
ID O25366_HELPY PRELIMINARY; PRT; 476 AA.
AC O25366;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006; entry version 25.
DE Fucosyltransferase.
GN OrderedLocusNames=HP0651; ORFNames=HP 0651;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1];
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Klenk H.-P., Gill S.R.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori."
RL Nature 388:539-547(1997).
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CC -----
DR EMBL; AB000511; AAD07710.1; -; Genomic_DNA.
DR PIR; C64601; C64601.
DR TIGR; HP0651; -.
DR LinkHub; O25366; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glycosyltransferase; Transferase.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 476 AA; 55927 MW; 32BFFDBBD361F74 CRC64;

Query Match 86.2%; Score 2058.5; DB 2; Length 476;
Best Local Similarity 84.5%; Pred. No. 2.4e-126;
Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

QY 1 MFQPLLDAYVESASIEKMAKSKS-PPPLKIVANWNGDEBEIKFKSVLYFIFSQRVITIAL 59
Db 1 MFQPLLDAYVESASIEKMAKSKSPPPLKIVANWNGDEBEIKFKSVLYFIFSQRVITIAL 60
QY 60 HQNPNEFSDLVFSPNPLGSAARKILSYQNTKRVFTYTGENSESPNLFDAIGFDELDPRDRY 119
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Db 61 HQNPNEFSDLVFSPNPLGSAARKILSYQNTKRVFTYTGENSESPNLFDAIGFDELDPRDRY 120
QY 120 LRMPLYYDRLHKKAESVNDTSPYKLNKNSLYTLKKPSHQFKENHPNLCVAVNDESDPLK 179
Db 121 LRMPLYYLAHLHYEAEVLVNDTTPAYKLNKNSLYALKKPSHHFKENHPNLCVAVNDESDLLK 180
QY 180 RGWVSFVASNANAPVRNAFYDALNSIEPVTGGSGVNTLGVNVKNKSEFSLQYKFNLCFE 239
Db 181 RGFASFVASNANAPVRNAFYDALNSIEPVTGGSGVNTLGVNVKNKSEFSLQYKFNLCFE 240
QY 240 NSQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNFKPFVNVHDFNNFDEADYIKYLHT 299
Db 241 NSQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNFKPSFNVHDFNNFDEADYIKYLHT 300
QY 300 HPNAVLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIYHKSSSTSFNWECDLDE 359
Db 301 HPNAVLDMLYENPLNLTDGKAYFYQDLSFKKILDFPKTILENDTIYH--NNPFIYRDLH 358
QY 360 EPLASI-----DDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 391
Db 359 EPLSIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 418
QY 392 NYDDLVRVNYDDLVRVNYERLLQNASPLLELSQNTSPKIYRKAYOKPI 437
Db 419 NYDDLVRVNYDDLVRVNYERLLQNASPLLELSQNTTFKIYRKAYOKSL 464

RESULT 3
O25142_HELPY
ID O25142_HELPY PRELIMINARY; PRT; 425 AA.
AC O25142;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Fucosyltransferase.
GN OrderedLocusNames=HP0379; ORFNames=HP 0379;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1];
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Klenk H.-P., Gill S.R.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori."
RL Nature 388:539-547(1997).
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CC -----
DR EMBL; AB000511; AAD07447.1; -; Genomic_DNA.
DR PIR; C64567; C64567.
DR TIGR; HP0379; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glycosyltransferase; Transferase.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;
```

Query Match 82.6%; Score 1972.5; DB 2; Length 425;
Best Local Similarity 85.8%; Pred. No. 8.7e-121;
Matches 376; Conservative 9; Mismatches 24; Indels 29; Gaps 2;

QY 1 MPQPLLDAYVESASIEKMASKS-PPPLKIANVWGDDEIKFKSVLYFIFISQRYTIAL 59
DB 1 MPQPLLDAYVESASIEKMASKSPPPLKIANVWGDDEIKFKSVLYFIFISQRYTIAL 60

QY 60 HONPNFSDLVFSPNPLGSAKILSYQNAKRVYTGGENEVPNPNLFDYAIGFDELDFRDR 119
DB 61 HONPNFSDLVFSPNPLGSAKILSYQNAKRVYTGGENEVPNPNLFDYAIGFDELDFRDR 120

QY 120 LRMPLYDRLHKAESVNDTTSFYKLKNSLYTLKKPSHQPKENHPNLCVAVNDESDPLK 179
DB 121 LRMPLYDRLHKAESVNDTTSFYKLKNSLYTLKKPSHQPKENHPNLCVAVNDESDPLK 180

QY 180 RGVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCF 239
DB 181 RGVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCF 240

QY 240 NSQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKEFVNVHDFNFDDEADYIKYLHT 299
DB 241 NSQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKEFVNVHDFNFDDEADYIKYLHT 300

QY 300 HPNAVLDMLYENPLNALDGKAYFYQDLGKILAFKTKILENDTIYHKSSTSFWMWECDDL 359
DB 301 HPNAVLDMLYENPLNALDGKAYFYQDLGKILAFKTKILENDTIYHKSSTSFWMWECDDL 360

QY 360 EPLASIDRLVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 419
DB 361 KPLVSDIDRLVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 420

QY 420 LSQNTSPFKIYKAYOKPI 437
DB 393 LSQNTTFKIYKAYOKSL 410

RESULT 4
Q9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
AC Q9ZLI3;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA (1,3)-FUCOSYLTRANSFERASE.
GN Name=fuct; ORFNames=jhp_0596;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives G.F.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
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CC
CC EMBL; AE001439; J05966; MONOMER; -.
DR BioCyc; HPYL85963:JHP0596-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.

DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;

Query Match 82.1%; Score 1959.5; DB 2; Length 454;
Best Local Similarity 83.2%; Pred. No. 6.7e-120;
Matches 371; Conservative 25; Mismatches 37; Indels 13; Gaps 4;

QY 1 MPQPLLDAYVESASIEKMASKSPPPLKIANVW--GDEIKFKSVLYFIFISQRYTIA 58
DB 1 MPQPLLDAYTDSRLDETGYK--PPLNIALANWPLDKRESKGFRRFIFILFSQRYTIT 58

QY 59 LHQNPNEFSDLVFSPNPLGSAKILSYQNAKRVYTGGENEVPNPNLFDYAIGFDELDFRDR 118
DB 59 LHQNPNEFSDLVFSPNPLGSAKILSYQNAKRVYTGGENEVPNPNLFDYAIGFDELDFRDR 118

QY 119 YLRMPLYDRLHKAESVNDTTSFYKLKNSLYTLKKPSHQPKENHPNLCVAVNDESDPL 178
DB 119 YLRMPLYDRLHKAESVNDTTSFYKLKNSLYTLKKPSHQPKENHPNLCVAVNDESDPL 178

QY 179 KRGVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCF 238
DB 179 KRGVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCF 238

QY 239 ENSQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKEFVNVHDFNFDDEADYIKYLH 298
DB 239 ENTQGYGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKEFVNVHDFNFDDEADYIKYLH 298

QY 299 THPNAYLDMLYENPLNALDGKAYFYQDLGKILAFKTKILENDTIYHKSSTSFWMWECDDL 358
DB 299 THPNAYLDMLYENPLNALDGKAYFYQDLGKILAFKTKILENDTIYHKSSTSFWMWECDDL 358

QY 359 DEPLASI-----DDLRYNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 411
DB 357 NEPLVAIDLRYNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 416

QY 412 QNASPLLELSQNTSFKIYKAYOKPI 437
DB 417 QNASPLLELSQNTTFKIYKAYOKSL 442

RESULT 5
Q9ZKD7_HELPJ PRELIMINARY; PRT; 436 AA.
AC Q9ZKD7;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA (1,3)-FUCOSYLTRANSFERASE.
GN Name=fucU; ORFNames=jhp_1002;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives G.F.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
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CC EMBL; AE001439; J05966; MONOMER; -.
DR BioCyc; HPYL85963:JHP0596-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.

DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 436 AA; 50699 MW; 1DB2066AE98FA61E CRC64;

Query Match 80.3%; Score 1917; DB 2; Length 436;
Best Local Similarity 83.1%; Pred. No. 3.8e-117; Indels 20; Gaps 4;
Matches 365; Conservative 20; Mismatches 34;

Qy 1 MFQPLLDAYVESASIERWAS--KSPPLKIAVANWGWDEEIKFKKSYLYFIFSQRYTIA 58
Db 1 MFQPLLDAYVESASIERWAS--KSPPLKIAVANWGWDEEIKFKKSYLYFIFSQRYTIA 58

Qy 59 LHQNPESDLVFNPIGSAKILSYQNAKRVFTGENEVPNFNLFDAIGFDELDFRDR 118
Db 59 LHQNPESDLVFNPIGSAKILSYQNAKRVFTGENEVPNFNLFDAIGFDELDFRDR 118

Qy 119 YLRMPLYADRLHKAESVNDTTSYKDKNSLYTLKPSHQFKENHPNLCVAVNDESPL 178
Db 119 YLRMPLYADRLHKAESVNDTTSYKDKNSLYTLKPSHQFKENHPNLCVAVNDESPL 178

Qy 179 KRGVSVFASVANAPMENAFAFDALNSIEPTVGGSVKNTLGYNVKNSSEFLSQYKFNLCF 238
Db 179 KRGVSVFASVANAPMENAFAFDALNSIEPTVGGSVKNTLGYNVKNSSEFLSQYKFNLCF 238

Qy 239 ENSQGYVTEKILDVFSHTPIYWGSPSVAKDFNPKFVNVDHFNDFDAIDYIKYLH 298
Db 239 ENSQGYVTEKILDVFSHTPIYWGSPSVAKDFNPKFVNVDHFNDFDAIDYIKYLH 298

Qy 299 THPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFKFTILENDTIYHKSSTSF 358
Db 299 THPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFKFTILENDTIYHKSSTSF 358

Qy 359 DEPLASIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 418
Db 359 DEPLASIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 418

Qy 419 ELSQNTSFKIYRKAYQKPI 437
Db 403 ELSQNTSFKIYRKAYQKSL 421

RESULT 6
Q6ST35_HELPY PRELIMINARY; PRT; 432 AA.
AC Q6ST35;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Alpha-1,4 fucosyltransferase.
GN Name=fucTII;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 6709;
RX PubMed=16000696; DOI=10.1093/glycob/cwj004;
RA Rabbani S., Miksa V., Wipf B., Ernst B.;
RT "Molecular Cloning and Functional Expression of a Novel Helicobacter
pylori [alpha]-1,4 Fucosyltransferase.";
RL Glycobiology 15:1076-1083 (2005).
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CC
CC EMBL; AY450598; AAR8243.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;

Query Match 79.3%; Score 1894.5; DB 2; Length 432;
Best Local Similarity 81.3%; Pred. No. 1.1e-115;
Matches 356; Conservative 30; Mismatches 33; Indels 19; Gaps 4;

Qy 1 MFQPLLDAYVESASIERWASPPPLKIAVANWGWDEEIKFKKSYLYFIFSQRYTIALH 60
Db 1 MFQPLLDAYIDSTLDLTDYK--PPLKIAVANWGWG--VEEFKSTLYFIFLSQRYTITLH 56

Qy 61 QNPNEFSDLVFNPIGSAKILSYQNAKRVFTGENEVPNFNLFDAIGFDELDFRDRYL 120
Db 57 RNPDKPADIVFGNPIGSAKILSYQNAKRVFTGENEVPNFNLFDAIGFDELDFRDRYL 116

Qy 121 RMPLYYDRLHKAESVNDTTSYKDKNSLYTLKPSHQFKENHPNLCVAVNDESPLKR 180
Db 117 RMPLYYAHLYEAEVLVNDTTSYKDKNSLYALKKPSHHFKENHPNLCVAVNDESPLKR 176

Qy 181 GVSFVASNANAPMENAFAFDALNSIEPTVGGSVKNTLGYNVKNSSEFLSQYKFNLCFEN 240
Db 177 GFASFVASNPAPKRNFAFDALNSIEPTVGGSVKNTLGYNVKNSSEFLSQYKFNLCFEN 236

Qy 241 SOGYGVTEKILDVFSHTPIYWGSPSVAKDFNPKFVNVDHFNDFDAIDYIKYLH 300
Db 237 SOGYGVTEKILDVFSHTPIYWGSPSVAKDFNPKFVNVDHFNDFDAIDYIKYLH 296

Qy 301 PNAYLDMLYENPLNADGKAYFYQDLSFKKILAFKFTILENDTIYHKSSTSF--MWECDLD 359
Db 297 PNAYLDMLYENPLNADGKAYFYQNLSPFKILDFKFTILENDTIYHCDAHNYSALHRLDN 356

Qy 360 EPLASIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLE 419
Db 357 EPLVSI-----DDLRYNDDLRINYDDLRINYDDLRINYERLLQNASPLLE 402

Qy 420 LSQNTSFKIYRKAYQKPI 437
Db 403 LSQNTSFKIYRKAYQKSL 420

RESULT 7
Q9L8S4_HELPY PRELIMINARY; PRT; 462 AA.
AC Q9L8S4;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 2.
DT 07-FEB-2006, entry version 17.
DE Alpha-1,3/4-fucosyltransferase.
GN Name=fucT4;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RX MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RT "Cloning and characterization of the alpha (1,3/4) fucosyltransferase
of Helicobacter pylori.";
RL J. Biol. Chem. 275:4988-4994 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucoyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F9B351ECB752 CRC64;

Query Match 75.9%; Score 1812.5; DB 2; Length 462;
Best Local Similarity 76.2%; Pred. No. 2.8e-110;
Matches 346; Conservative 33; Mismatches 54; Indels 21; Gaps 5;

Qy 1 MFQPLDVAVFESASTKMAKSPPLKATAVANW--GDEEIKFKKSVLYFIFSORYTIA 58
Db 1 MFQPLDVAFDISTHDETHK--PPLVALANWPLKSEKKGKGFDFILHFLKQRYKII 58

Qy 59 LHQNPNEFSDLVFNSPLGSAKILSYQNAKRVFYTTGENEVPNPNLFDYAIGFDELDFRDR 118
Db 59 LHSNPNESDLVFGNPLQARILSYQNTKRVFYTTGENEVPNPNLFDYAIGFDELDFRDR 118

Qy 119 YLRMPLYDRLHKKAESVNDTTPYKLDKNSLYTLKKGSHQPKENHPNLCVAVNDESDPL 178
Db 119 YLRMPLYAYLHYKAMLVNDTTPYKLDK--ALYTLKKGSHKPKENHPNLCALIHNESDPW 176

Qy 179 KRGVVSFVASANAPMNAFADALNSIEPVTGGGSKVNTLGYNVKNKSEFLSOYKFNLCF 238
Db 177 KRGFASFVASNPNAPIRAFADALNAIEFVAGSGVSKNTLGYNVKNKSEFLSOYKFNLCF 236

Qy 239 ENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIKYLH 298
Db 237 ENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLH 296

Qy 299 THPNAYDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIYHKSTSP-MWBCD 357
Db 297 AHQNAVYDMLYENPLNTIDGKAGFYQDLSFKKILDFKFNILENDTIYHCNDAHYGALHRED 356

Qy 358 LDEPLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 407
Db 357 LNEPLVSVDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 416

Qy 408 ---ERLLQNASPLLELSQNTSFKIYKAYOKPI 437
Db 417 RDHERLSKATPLLELSQNTSFKIYKAYOKSL 450

RESULT 8
O32631_HELPY PRELIMINARY; PRT; 333 AA.
AC O32631;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Alpha-(1,3)-fucoyltransferase (EC 2.4.1.-).
GN Name=fuci;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11637;
RX MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Eijnden D.H.,
RA Bird M.I.;
RT "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
RT alpha(1,3)-fucoyltransferase gene."
RL J. Biol. Chem. 272:21349-21356(1997).
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DR EMBL; AF006039; AAB93985.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucoyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFFCB1AC127E0A8C CRC64;

Query Match 62.9%; Score 1502.5; DB 2; Length 333;
Best Local Similarity 86.4%; Pred. No. 3.7e-90;
Matches 279; Conservative 19; Mismatches 16; Indels 9; Gaps 2;

Qy 122 MPLYDRLHKKAESVNDTTPYKLDKNSLYTLKKGSHQPKENHPNLCVAVNDESDPLKRG 181
Db 1 MPLYDRLHKKAESVNDTTPYKLDKNSLYTLKKGSHQPKENHPNLCALINNESDPLKRG 60

Qy 182 VVSFVASNANAPMNAFADALNSIEPVTGGGSKVNTLGYNVKNKSEFLSOYKFNLCFENS 241
Db 61 FASFVASNANAPMNAFADALNSIEPVTGGGAVKNTLGYNVKNKSEFLSOYKFNLCFENS 120

Qy 242 QGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIKYLTHP 301
Db 121 QGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYVRYLTHP 180

Qy 302 NAYDMLYENPLNALDGKAYFYQDLSFKKILAFPKTILENDTIYHKSTSPFMWECDLDEP 361
Db 181 NAYDMLYENPLNTIDGKAYFYQDLSFKKILDFPKTILENDTIYH--NNPFIYRDLNDEP 238

Qy 362 LASI-----DGLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 414
Db 239 LVSIDMLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 298

Qy 415 SPLELSQNTSFKIYKAYOKPI 437
Db 299 SPLELSQNTSFKIYKAYOKSL 321

RESULT 9
Q5L9S6_BACFN PRELIMINARY; PRT; 331 AA.
AC Q5L9S6;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative LPS biosynthesis related glycosyltransferase.
GN OrderedLocusNames=BF3460;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Foxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression."
RL Science 307:1463-1465(2005).
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CC
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EMBL; CR626927; CAH09151.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008417; F:fucoyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.

DR InterPro; IPR002105; Dockerin_1.

Qy 273 FNPKE-FVNVHDFNNFDEADYIKYLHFNNA-VLDMLYENPLALDCKAFYFDLSFKK 333
 Db 279 FIPENTFIDKFNFSNYE---DLVLYLRKMPDGEYLYKL-ENIENYLNSE-----QSLQPKS 330
 Qy 331 ILAPFKFILE 340
 Db 331 -EGFVQIVVQ 339
 RESULT 13
 Q54PH9 DICDI
 ID Q54PH9 DICDI PRELIMINARY; PRT; 389 AA.
 AC Q54PH9;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-MAR-2006, entry version 5.
 DE Hypothetical protein fut1.
 DE Hypothetical protein fut1.
 GN Name=fut1; ORFNames=DDB0219943;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RC PubMed=15875012; DOI=10.1038/nature03481;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
 RA Sugchang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hanlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzy D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
 RA Buchrieser C., Wardrop A., Feider M., Thangavelu M., Johnson D.,
 RA Knights A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
 RA Tivey A., Sugano S., White B., Walker D., Woodcock J.R., Winckler T.,
 RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrrell B.G.,
 RA Kuspa A.;
 RA "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 435:43-57 (2005).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC
 CC EMBL; AAFI01000108; EAL65160.1; -; GenBmic_DNA.
 CC GO; GO:0016020; C:membrane; IEA.
 CC GO; GO:0008417; F:fucosyltransferase activity; IEA.
 CC GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 CC InterPro; IPR001503; Glyco trans 10.
 CC DR PANTHER; PTHR11929; Glyco_trans_10; 1.
 CC KW Glycosyltransferase; Golgi stack; Hypothetical protein; Transferase;
 CC Transmembrane.
 CC SEQUENCE 389 AA; 45383 MW; 9EA7D88C3D423F99 CRC64;
 Query Match 8.1%; Score 192.5; DB 2; Length 389;
 Best Local Similarity 24.6%; Pred. No. 0.00024;
 Matches 88; Conservative 70; Mismatches 131; Indels 69; Gaps 20;
 Qy 7 DAYVESASIEKMASK-SPPLKIVANWMDDEETKEPKSVLFIFSQRYTIALHQPNNE 65
 Db 48 DNYFNKEVNESFSKCKPKCKIEHSEFSNEK-ASAQAIIYF-FSQY-----QE 96
 Qy 66 FSDLVFSNPLIG--SARKIL---SYQNAKRVFYTGENE--VPNFNLFYATGFDEL-DFRD 117

Db 97 SSKNYNTLKRYPNROITIGTWTESGGLYRFGSDSNFIISNFNI---TVGYPVNDVFNK 153
Qy 118 R---YLRM-PLY---DRLHHKASVNDTSPYKLDNSLYTLKKPSHQKFNHPNLCV 170
Db 154 QTHIYVYGFVEYSGSDSYAHSKAFRIKIPSK-RNNSIVWIS--SNCWHEDY----- 204
Qy 171 VNDESDELKGVSVFVASNANAPRNAPYDALNSIEPVTGGSVKNTLGYNVKNKSFLS 230
Db 205 -----KR--VYLMRSINWITKVDYSGCLNID-FTQDQKLINS---KHDQKMDVLK 250
Qy 231 QYFNLFCFNSQGYGYVTEKILDYFHSHTPIYWGSPSVAKDF-NPKFVNVHDFNPFDE 289
Db 251 RYNFAIAFNSLCKDYITEKLVESLSVGTPIYLGAPNIMEFLPDPDSIINVRDFKSVND 310
Qy 290 AIDYIKVLHPTHNAYLDML-----YENPLNALDGKAYFYQDLSFKKIL 332
Db 311 LVDIYIKKVVENDONLRLKHLKWKIKKWSKBFQNIYDESVANLDPCLCSKIASKIL 368

RESULT 14
Q54F09_DICDI
ID Q54F09_DICDI PRELIMINARY; PRT; 462 AA.
AC Q54F09;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=DDB0186041;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriam M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., In M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulsegged H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC
CC -----
CC EMBL; AAF10100108; EAL65179.1; -; Genomic_DNA.
CC DR GO; GO:0016020; C:membrane; IEA.
CC DR GO; GO:0008417; P:fucosyltransferase activity; IEA.
CC DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
CC DR PANTHER; PTHR11929; GlycoTrans 10.
CC DR KW Glycosyltransferase; Golgi stack; Hypothetical protein; Transferase;
CC TRANSMEMBRANE
CC SEQUENCE 462 AA; 54815 MW; 444843FFBAE6FD77 CRC64;

Query Match 8.0%; Score 191.5; DB 2; Length 462;
Beat Local Similarity 25.6%; Pred. No. 0.00034;
Matches 75; Conservative 50; Mismatches 105; Indels 63; Gaps 14;
Qy 48 YPIFSQRYTIALHQNPNF-----FSDLV---FSNPLGSAKILSYONAKRVPYTTGENEVP 99
Db 131 YVIVRKPY-----YPNQKLDMEIWSYIVDFEAP-----KKKLSRNVPRTLISMEPO-P 179
Qy 100 N-----FNLFDYALGPD-ELDFRDYLRMLPLYDRLHHKASVNDTSPYKLDN- 148
Db 180 NRTCEPKDCEFFENFKVSFESQSDIR-----MGPD-----TPSSSAYKLYNKL 223
Qy 149 SLTYLTKPSPHOFKENHP-----NLCAVNVNDESDPLKRGVSVFVASNANAPRNAPYDALNS 204
Db 224 TIDEIAKIQTQKLEYQVMKINNTLQPHQKSIPLANWFCTNCNSHN---RNEYVQELMK 280
Qy 205 IEPVTG-GGSVKNT-----LGVNVNKSEFLSQYKFNLCFNSQGYGYVTEKILDA 254
Db 281 FIVVDSFGKCLKNMPTSNFLSRGSGDPPERKRLFITRYKFTIVFENSICKDYVSEKVLDA 340
Qy 255 YFSHTPIYWGSPSVAKDFNPKFVNVHDFNPFDEAIDYIKVLHPTHNAYLDM 307
Db 341 LIAGSVPIFMGHPSTIKYPLNSYIFVGVDFKNAEHLNHLKFLSENDNEYFKL 393

RESULT 15
Q54L56_DICDI
ID Q54L56_DICDI PRELIMINARY; PRT; 665 AA.
AC Q54L56;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=DDB0187176;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriam M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC -----
CC EMBL; AAF101000141; EAL64002.1; -; Genomic_DNA.
CC DR GO; GO:0016020; C:membrane; IEA.
CC DR GO; GO:0008417; P:fucosyltransferase activity; IEA.
CC DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
CC DR PANTHER; PTHR13320; ConA like subgrp.
CC DR InterPro; IPR001503; GlycoTrans 10.
CC SEQUENCE 665 AA; 72480 MW; 444843FFBAE6FD77 CRC64;

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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:45:14 ; Search time 30.5753 Seconds
(without alignments)
1276.805 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 2388

Sequence: 1 MFQPLLDAYVESASIERKMAS.....KIYKAYQKPIKNPPYPYCAP 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	87.4	464	2	US-09-092-315-1
2	2086	87.4	464	2	US-09-733-524A-1
3	2086	87.4	464	2	US-10-189-977A-1
4	2086	87.4	464	3	US-10-392-098A-1
5	2079	87.1	478	2	US-09-733-524A-7
6	2079	87.1	478	2	US-10-189-977A-7
7	2079	87.1	478	3	US-10-392-098A-7
8	2073	86.8	478	2	US-09-092-315-7
9	2070.5	86.7	454	2	US-09-092-315-8
10	2070.5	86.7	454	2	US-09-733-524A-8
11	2070.5	86.7	454	2	US-10-189-977A-8
12	2070.5	86.7	454	3	US-10-392-098A-8
13	2058.5	86.2	476	2	US-09-092-315-5
14	2058.5	86.2	476	2	US-09-733-524A-5
15	2058.5	86.2	476	2	US-10-189-977A-5
16	2058.5	86.2	476	3	US-10-392-098A-5
17	2036	85.3	486	2	US-09-092-315-2
18	2036	85.3	486	2	US-09-733-524A-2
19	2036	85.3	486	2	US-10-189-977A-2
20	2036	85.3	486	3	US-10-392-098A-2
21	1972.5	82.6	425	2	US-09-092-315-6
22	1972.5	82.6	425	2	US-09-733-524A-6
23	1972.5	82.6	425	2	US-10-189-977A-6
24	1972.5	82.6	425	3	US-10-392-098A-6
25	1861	77.9	440	2	US-09-092-315-3
26	1861	77.9	440	2	US-09-733-524A-3

27	1861	77.9	440	2	US-10-189-977A-3	Sequence 3, Appli
28	1861	77.9	440	3	US-10-392-098A-3	Sequence 3, Appli
29	1812	75.9	372	2	US-09-092-315-13	Sequence 13, Appl
30	528	22.1	502	2	US-10-080-960-16	Sequence 16, Appl
31	188	7.0	36	2	US-09-092-315-14	Sequence 14, Appl
32	168	7.0	36	2	US-09-733-524A-14	Sequence 14, Appl
33	168	7.0	36	2	US-10-189-977A-14	Sequence 14, Appl
34	168	7.0	36	3	US-10-392-098A-14	Sequence 14, Appl
35	149.5	6.3	139	2	US-10-080-960-18	Sequence 18, Appl
36	145.5	6.1	486	2	US-10-080-960-2	Sequence 2, Appli
37	141.5	5.9	433	2	US-09-092-315-11	Sequence 11, Appl
38	141.5	5.9	433	2	US-09-733-524A-11	Sequence 11, Appl
39	141.5	5.9	433	2	US-10-189-977A-11	Sequence 11, Appl
40	141.5	5.9	433	3	US-10-392-098A-11	Sequence 11, Appl
41	141	5.9	915	2	US-09-583-110-3100	Sequence 3100, Ap
42	126.5	5.3	365	2	US-09-733-524A-9	Sequence 9, Appli
43	126.5	5.3	365	2	US-10-189-977A-9	Sequence 9, Appli
44	125.5	5.3	365	2	US-09-092-315-9	Sequence 9, Appli
45	125.5	5.3	365	2	US-09-390-131-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-092-315-1
; Sequence 1, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; EARLIER FILING DATE: 1998-06-05
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-1

Query Match 87.4%; Score 2086; DB 2; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.6e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

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DB	1	MFQPLLDAYVESASIERKMASPPPLKIAVANWGWGDEEIKPKKSVLYFIFFSORYTIALH	60
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DB	61	QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNFNLFDAIGAIFDELDFDRYL	120
QY	121	RMPLYYDRLHKAESVNDTTSYKKNLSYTLTKPKSHQPKENHNLCAVVDNEDSPDKR	180
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QY	181	GVVSFVSNANAPMNAFYDALNSIEPTVGGGSKVNTLGVNVKNKSEFLSOYKFNLCFEN	240
DB	181	GVVSFVSNANAPMNAFYDALNSIEPTVGGGSKVNTLGVNVKNKSEFLSOYKFNLCFEN	240
QY	241	SGYGVVTEKILDAYFSHTPIYWGSPSVAKDPNPKFVNVHDFNNFDEAIDYIKYLHHT	300
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QY	301	PNAYLDMLYENPLNADGKAYFYQDLSPFKKILAFFKXITLLENDTIYHKSTSFWMWCDLDE	360
DB	301	PNAYLDMLYENPLNADGKAYFYQDLSPFKKILAFFKXITLLENDTIYHKSTSFWMWCDLDE	360

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QY 361 PLASIDDLRV-----NYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 406
Db 359`PLVTIDDLRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 418
QY 407 YERLLQNAPLLELSQNTSKYRKAYQKPI 437
Db 419 YERLLSKATPLLELSQNTSKYRKAYQKSL 449

RESULT 2
US-09-733-524A-1
; Sequence 1, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-1

Query Match 87.4%; Score 2086; DB 2; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.6e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

QY 1 MFQPLLDAYVESASIERKASVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 120
Db 1 MFQPLLDAYVESASIERKASVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 120
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Db 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVPYTGNEVPNPNLFDYAGFDELDFRDYL 120
QY 121 RMPLYYDLRHKAESVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 180
Db 121 RMPLYYDLRHKAESVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 180
QY 181 GVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVNTLGYNVKNKSEFLSQYKFNLCFEN 240
Db 181 GVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVNTLGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SQGYGYVTEKILDYFHSHTIPYWGSPSVAKDFNPKFVNVHDFNNDFAIDYIKYLH 300
Db 241 TQGYGYVTEKIIDAYFSHTIPYWGSPSVAKDFNPKFVNVHDFNNDFAIDYIKYLH 300
QY 301 PNAVLDMLYENPLNLDGKAYFYQDLSPFKILAFKTLILENDTIYHKSSTSFMECDLDE 360
Db 301 KNAVLDMLYENPLNLDGKAYFYQDLSPFKILAFKTLILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 406
Db 359`PLVTIDDLRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 418
QY 407 YERLLQNAPLLELSQNTSKYRKAYQKPI 437
Db 419 YERLLSKATPLLELSQNTSKYRKAYQKSL 449

RESULT 3
US-10-189-977A-1
; Sequence 1, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-1

Query Match 87.4%; Score 2086; DB 2; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.6e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

QY 1 MFQPLLDAYVESASIERKASVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 120
Db 1 MFQPLLDAYVESASIERKASVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 120
QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVPYTGNEVPNPNLFDYAGFDELDFRDYL 120
Db 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVPYTGNEVPNPNLFDYAGFDELDFRDYL 120
QY 121 RMPLYYDLRHKAESVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 180
Db 121 RMPLYYDLRHKAESVNDTTPYKLNKSLYTLKPKSHQPKENHPNLCVAVNDESDPLKR 180
QY 181 GVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVNTLGYNVKNKSEFLSQYKFNLCFEN 240
Db 181 GVSVFVSNANAPRNAPFYDALNSIEPTVGGSGVNTLGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SQGYGYVTEKILDYFHSHTIPYWGSPSVAKDFNPKFVNVHDFNNDFAIDYIKYLH 300
Db 241 TQGYGYVTEKIIDAYFSHTIPYWGSPSVAKDFNPKFVNVHDFNNDFAIDYIKYLH 300
QY 301 PNAVLDMLYENPLNLDGKAYFYQDLSPFKILAFKTLILENDTIYHKSSTSFMECDLDE 360
Db 301 KNAVLDMLYENPLNLDGKAYFYQDLSPFKILAFKTLILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 406
Db 359`PLVTIDDLRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 418
QY 407 YERLLQNAPLLELSQNTSKYRKAYQKPI 437
Db 419 YERLLSKATPLLELSQNTSKYRKAYQKSL 449
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; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11639
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-1

Query Match      87.4%; Score 2086; DB 3; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.6e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFISQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFISQRYTIALH 60

QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTYGTGENEVPNLFYDVAIGFDELDNDRYL 120
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTYGTGENEVPNLFYDVAIGFDELDNDRYL 120

QY 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180
DB 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180

QY 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180
DB 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180

QY 181 GVVSFVASNANAPRNAPAFYDALNSIEPVTGGSGVNTLGYNVKNKSEFLSOYKFNLCFEN 240
DB 181 GFASFVSNAPRNAPAFYDALNSIEPVTGGSGVNTLGYNVKNKSEFLSOYKFNLCFEN 240

QY 241 SQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNNDFAIDYIKYLH 300
DB 241 TQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNNDFAIDYIKYLH 300

QY 301 PNAYLDMLENPLNADGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMECDLDE 360
DB 301 KNAVLDMLYENPLNADGKAYFYQDLSFKKILAFFKTILENDTIYH--DNPFIFCRDLNE 358

QY 361 PLASIDDLRV-----NYDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVN 406
DB 359 PLVTIDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVN 418

QY 407 YERLLQNASPLLELSQNTSFKIYKAYQKPI 437
DB 419 YERLLSKATPILLELSQNTTSKIYKAYQKSL 449
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RESULT 5

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US-09-733-524A-7
; Sequence 7, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
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; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-7

Query Match      87.1%; Score 2079; DB 2; Length 478;
Best Local Similarity 84.7%; Pred. No. 7.9e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFISQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFISQRYTIALH 60

QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTYGTGENEVPNLFYDVAIGFDELDNDRYL 120
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTYGTGENEVPNLFYDVAIGFDELDNDRYL 120

QY 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180
DB 121 RMPLYYDRLHHKAEVNDTTPYKLDKNSLYTLKPSHQPENHNPNCVAVNDESDPLKR 180

QY 181 GVVSFVASNANAPRNAPAFYDALNSIEPVTGGSGVNTLGYNVKNKSEFLSOYKFNLCFEN 240
DB 181 GFASFVSNAPRNAPAFYDALNSIEPVTGGSGVNTLGYNVKNKSEFLSOYKFNLCFEN 240

QY 241 SQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNNDFAIDYIKYLH 300
DB 241 TQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNNDFAIDYIKYLH 300

QY 301 PNAYLDMLENPLNADGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMECDLDE 360
DB 301 KNAVLDMLYENPLNADGKAYFYQDLSFKKILAFFKTILENDTIYH--DNPFIFCRDLNE 358

QY 361 PLASIDDLRV-----NYDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVN 392
DB 359 PLVTIDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVNYDDLRYNDDLRVN 418

QY 393 YDDLRYNDDLRVNYERLLQNASPLLELSQNTSFKIYKAYQKPI 437
DB 419 YDDLRYNDDLRVNYERLLSKATPILLELSQNTTSKIYKAYQKSL 463
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RESULT 6

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US-10-189-977A-7
; Sequence 7, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-7
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Query Match      87.1%; Score 2079; DB 2; Length 478;
Best Local Similarity 84.7%; Pred. No. 7.9e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
QY 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
QY 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
DB 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
QY 181 GVSVFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GFASFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SQGGYVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFNNFDEAIDYIKYLH 300
DB 241 TQGGYVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFNNFDEAIDYIKYLH 300
QY 301 PNAVLDMLYENPLNADGKAYFYODLSFKKTLAPFKTILENDTIYHKSSTSPFWECDLDE 360
DB 301 KNAVLDMLYENPLNADGKAYFYODLSFKKTLAPFKTILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLRYNDDLRVNYDDLRINYYDDLRYNDDLRVNYDDLRIN 392
DB 359 PLVTIDDLRVNYDDLRVNYDDLRINYYDDLRYNDDLRVNYDDLRVNYDDLRIN 418
QY 393 YDDLRYNDDLRVNYERLLQNASPLLELSQNTSKYKAYOKPI 437
DB 419 YDDLRYNDDLRVNYERLLSKATPLLELSQNTSKYKAYOKSL 463

RESULT 7
US-10-392-098A-7
; Sequence 7, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11639 (763)
US-10-392-098A-7

Query Match      87.1%; Score 2079; DB 3; Length 478;
Best Local Similarity 84.7%; Pred. No. 7.9e-189;
Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
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DB 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
QY 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
DB 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
QY 181 GVSVFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GFASFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SQGGYVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFNNFDEAIDYIKYLH 300
DB 241 TQGGYVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFNNFDEAIDYIKYLH 300
QY 301 PNAVLDMLYENPLNADGKAYFYODLSFKKTLAPFKTILENDTIYHKSSTSPFWECDLDE 360
DB 301 KNAVLDMLYENPLNADGKAYFYODLSFKKTLAPFKTILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLRYNDDLRVNYDDLRINYYDDLRYNDDLRVNYDDLRIN 392
DB 359 PLVTIDDLRVNYDDLRVNYDDLRINYYDDLRYNDDLRVNYDDLRVNYDDLRIN 418
QY 393 YDDLRYNDDLRVNYERLLQNASPLLELSQNTSKYKAYOKPI 437
DB 419 YDDLRYNDDLRVNYERLLSKATPLLELSQNTSKYKAYOKSL 463

RESULT 8
US-09-092-315-7
; Sequence 7, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-7

Query Match      86.8%; Score 2073; DB 2; Length 478;
Best Local Similarity 84.5%; Pred. No. 2.9e-188;
Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKFKNSVLYFISQRYTIALH 60
QY 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
DB 61 QNPNEFSDLVFSGNPLGSAKILSYQNAKRVFTGTGENEVPNENLFDYAIGFDELDFDRYL 120
QY 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
DB 121 RMPLYYDRLLHKAESVNDTTPYKLNKNSLYTLKKPSHOFKENHPNLCAVAVNDESPLKR 180
QY 181 GVSVFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GFASFVASNAPMRNAPFYDALNSIEPTVGGGSKVNTLGYNVKNKSEFLSQYKFNLCFEN 240
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; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-8

Query Match 86.7%; Score 2070.5; DB 2; Length 454;
Best Local Similarity 86.5%; Pred. No. 4.7e-188;
Matches 384; Conservative 27; Mismatches 24; Indels 9; Gaps 2;

Qy 1 MFQPLLDAYVESASIERKASKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 60
Db 1 MFQPLLDAYVESASIERKASKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 60

Qy 61 QNPNEFDLVSPLGSAKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 120
Db 61 QNPNEFDLVSPLGSAKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 120

Qy 121 RMPLYDRLHKAESVNDTTPYKLNLSYTLKPKSHQFKNHPNLCVAVNDESPLKR 180
Db 121 RMPLYDRLHKAESVNDTTPYKLNLSYTLKPKSHQFKNHPNLCVAVNDESPLKR 180

Qy 181 GVSVFASVANAPMRNPFYDALNSIEPTVGGGSKNTLGYVKNKSEFLSQYKFNLCFEN 240
Db 181 GVSVFASVANAPMRNPFYDALNSIEPTVGGGSKNTLGYVKNKSEFLSQYKFNLCFEN 240

Qy 241 SQGYGVTEKILDYFSTHTPIYWGSPSAKDFNPKFVNVDHFNNDFAIDYIKYLH 300
Db 241 SQGYGVTEKILDYFSTHTPIYWGSPSAKDFNPKFVNVDHFNNDFAIDYIKYLH 300

Qy 301 PNAYLDMLYENPLNADGKAYFYQDLSPKKILAFKTLLENDTIYHKSSTSPFWECDDLE 360
Db 301 PNAYLDMLYENPLNADGKAYFYQDLSPKKILAFKTLLENDTIYH--NNPFIYTRDLNE 358

Qy 361 PLASI-----DRLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYERLQN 413
Db 359 PLVSDINLRINVDNLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYERLQN 418

Qy 414 ASPLLELSQNTSFKIYRKAYQKPI 437
Db 419 ASPLLELSQNTSFKIYRKAYQKSL 442

RESULT 12
US-10-392-098A-8
; Sequence 8, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: University of Alberta
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11637
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-8

Query Match 86.7%; Score 2070.5; DB 3; Length 454;
Best Local Similarity 86.5%; Pred. No. 4.7e-188;
Matches 384; Conservative 27; Mismatches 24; Indels 9; Gaps 2;

Qy 1 MFQPLLDAYVESASIERKASKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 60
Db 1 MFQPLLDAYVESASIERKASKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 60

Qy 61 QNPNEFDLVSPLGSAKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 120
Db 61 QNPNEFDLVSPLGSAKILSYONAKRVFTYTGNEVPNLFNFDYAI GFDELDFRDYL 120

Qy 121 RMPLYDRLHKAESVNDTTPYKLNLSYTLKPKSHQFKNHPNLCVAVNDESPLKR 180
Db 121 RMPLYDRLHKAESVNDTTPYKLNLSYTLKPKSHQFKNHPNLCVAVNDESPLKR 180

Qy 181 GVSVFASVANAPMRNPFYDALNSIEPTVGGGSKNTLGYVKNKSEFLSQYKFNLCFEN 240
Db 181 GVSVFASVANAPMRNPFYDALNSIEPTVGGGSKNTLGYVKNKSEFLSQYKFNLCFEN 240

Qy 241 SQGYGVTEKILDYFSTHTPIYWGSPSAKDFNPKFVNVDHFNNDFAIDYIKYLH 300
Db 241 SQGYGVTEKILDYFSTHTPIYWGSPSAKDFNPKFVNVDHFNNDFAIDYIKYLH 300

Qy 301 PNAYLDMLYENPLNADGKAYFYQDLSPKKILAFKTLLENDTIYHKSSTSPFWECDDLE 360
Db 301 PNAYLDMLYENPLNADGKAYFYQDLSPKKILAFKTLLENDTIYH--NNPFIYTRDLNE 358

Qy 361 PLASI-----DRLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYERLQN 413
Db 359 PLVSDINLRINVDNLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYERLQN 418

Qy 414 ASPLLELSQNTSFKIYRKAYQKPI 437
Db 419 ASPLLELSQNTSFKIYRKAYQKSL 442

RESULT 13
US-09-092-315-5
; Sequence 5, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-5

Query Match 86.2%; Score 2058.5; DB 2; Length 476;
Best Local Similarity 84.5%; Pred. No. 7e-187;

Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

Qy	1	MFQQLDAYVESASIEKWSKSS--DPPLKIAVANWGWDEDEIKEPFKSVLYFIPISQRYTIAL	59
Db	1	MFQQLDAYVESASIEKWSKSSPPPLKIAVANWGWDEDEIKEPFKSVLYFIIISQRYAITL	60
Qy	60	HQNPNEPFDLVFSNPLGSARKILSYQNAKRVPYFTGENEVPNPNLFDYALGFDELDPDRRY	119
Db	61	HQNPNEPFDLVFSNPLGAARKILSYQNTKRVFTYGENESPENLFDYALGFDELDFNDRY	120
Qy	120	LRMPLYYDRLHHKAESVNDTTSPYKLKDNLSIYTLKKPSHQFKENHPNLCAVNVNDSDDLK	179
Db	121	LRMPLYYAHLHYEAEALVNDTTAPYKLKDNLSIYALKKPSHHFKENHPNLCAVNVNDSDDLK	180
Qy	180	RGVVSFVASNANAEMRNAFYDALNSIIEPVTGGGSVKNTLGYNVKVKSEPLSOYKNLCPE	239
Db	181	RGFASFVASNANAEMRNAFYDALNSIIEPVTGGGSVRNTLGYGVKNSEPLSOYKNLCPE	240
Qy	240	NSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDNPKFNVNVDFFNNFDEAIDYIKYLHT	299
Db	241	NSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDNPKSFNVNVDFFNNFDEAIDYIKYLHT	300
Qy	300	HPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFPKTKILENDTIYHKSSSTSFMECEDLD	359
Db	301	HPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTKILENDTIYH--NNPFIYPRDLH	358
Qy	360	EPLASI-----DDLRVNYDDDLRVNYDDDLRVNYDDDLRVNYDDDLRV	391
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Db	419	NYDDLRVNYDDDLRVNYERLLQNASPLLELSQNTTFKIYRKAYQKSL	464

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RESULT 14
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUSOXYLITRANFRASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

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Query Match 86.2%; Score 2058.5; DB 2; Length 476;
Best Local Similarity 84.5%; Pred. No. 7e-187;
Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

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Qy	60	HQNPNE	SDLVFN	PLSG	ARKILSY	QNAKRV	YFTY	TGENE	VPNFNL	FDYAI	GEDELDFDRY	119
Db	61	HQNPNE	SSDLVFN	PLSG	ARKILSY	QNTKRV	YFTY	TGENE	SPNFNL	FDYAI	GEDELDFDRY	120
Qy	120	LRMPY	YDRLLH	KAES	VNDTTS	PKYK	XNSLSY	TLTKP	SHQFEN	HPNLCA	VVNDESDPLK	179

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180 RGVVSFVASNANAPRNAFYDALANSIEPVTGGGSVKNTLGVNVKNKSEFLSQYKFNLCFE 239
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360 EPLASI-----DLEVNVDLRLVNVYDDLRLVNVYDDLRLVNVYDDLRLV 391
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392 NYDDLRLVNVYDDLRLVNVYERLLQNAGSPLLELSONTSFKIYRKAYQKPI 437
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419 NYDDLRLVNVYDDLRLVNVYERLLQNAGSPLLELSONTSFTFKIYRKAYQKSL 464
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RESULT 15
US-10-189-977A-5
; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; TITLE OF INVENTION: EXPRESSING THEM (amended)

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, CURRENT APPLICATION NUMBER: US/10/189,977A
,
, CURRENT FILING DATE: 2002-03-07
,
, PRIOR APPLICATION NUMBER: US/09/733,524
,
, PRIOR FILING DATE: 2000-12-07
,
, PRIOR APPLICATION NUMBER: US 09/092,315
,
, PRIOR FILING DATE: 1998-06-05
,
, PRIOR APPLICATION NUMBER: US 60/048,857
,
, PRIOR FILING DATE: 1997-06-06
,
, NUMBER OF SEQ ID NOS: 27
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, SOFTWARE: FastSeq for Windows Version 4.0
,
, SEQ ID NO 5
,
, LENGTH: 476
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, TYPE: prt
,
, ORGANISM: Helicobacter pylori
,
, US-10-189-977A-5

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Query Match	86.2%	Score 2058.5	DB 2	Length 476
Best Local Similarity	84.5%	Pred. No. 7e-187		
Matches 394	Conservative	13	Mismatches 28	Indels 31
				Gaps 3

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				:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:															
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				:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:												
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Db	61	HQNP	E	S	D	L	V	F	N	S	P	L	G	A	R	K	I	L	S	Y	O	N	T	K	R	V	F	Y	T	G	E	N	E	S	P	N	F	N	L	F	D	Y	A	I	G	D	E	L	F	N	D	R	Y	120		
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Qy	120	LRMP	Y	Y	D	R	L	H	H	K	A	E	S	-	N	D	T	T	S	P	K	L	K	D	N	S	L	Y	T	L	K	P	-	S	H	Q	F	K	E	N	H	P	N	L	C	A	V	N	D	E	S	D	L	K	179	
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Db	121	LRMP	Y	Y	A	H	L	H	E	A	E	L	-	N	D	T	T	A	P	K	L	K	D	N	S	L	Y	A	L	K	P	-	S	H	H	F	K	E	N	H	P	N	L	C	A	V	N	D	E	S	D	L	K	180		
				:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:							
Qy	180	RGVV	S	F	V	A	S	A	N	A	P	M	R	N	A	F	D	A	L	N	S	I	E	P	V	T	G	G	S	V	K	N	T	L	G	Y	N	N	K	S	E	F	L	S	O	K	N	E	L	C	F	E	239			
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Db	181	RGF	A	S	F	V	A	S	A	N	A	P	M	R	N	A	F	D	A	L	N	S	I	E	P	V	T	G	G	S	V	R	N	T	L	G	Y	K	V	G	N	K	S	E	F	L	S	O	K	N	E	L	C	F	E	240
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Qy	240	NSQ	G	Y	G	V	V	T	E	K	I	L	D	A	F	E	S	T	I	P	I	Y	W	G	S	P	S	V	A	K	O	F	N	P	K	E																				

Db	241	NSQGYGVTEKILDVFSHTIPYWGSPSVAKDFNPKSFVNVHDFNFDIDAIDYIKYLHT	300
Qy	300	HPNAYLDMLYENPINALDGKAYFYQDLSFKKILAPFKTILENDTIYKSSTSFMWECOLD	359
Db	301	HPNAYLDMLYENPINALDGKAYFYQDLSFKKILAPFKTILENDTIYH--NNPFIYRDLH	358
Qy	360	EPLASI-----DDLRVNYDDLVRVNYDDLVRVNYDDLVRV	391
Db	359	EPLISIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV	418
Qy	392	NYDDLVRVNYDDLVRVNYERLLQNASPLLELSQNTSFKIYRKAYQKPI	437
Db	419	NYDDLVRVNYDDLVRVNYERLLQNASPLLELSQNTTTFKIYRKAYQKSL	464

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Job time : 31.5753 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:46:14 ; Search time 108.675 Seconds
(without alignments)
1901.022 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 2388

Sequence: 1 MFQPLLDAYVESASIEKMAS.....KIYKAYQKPIKNPVPYCAP 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2086	87.4	464	4	US-10-120-319-1
3	2086	87.4	464	4	US-10-189-977-1
4	2086	87.4	464	4	US-10-392-098-1
5	2079	87.1	478	4	US-10-392-098-7
6	2073	86.8	478	4	US-10-120-319-7
7	2073	86.8	478	4	US-10-189-977-7
8	2073	86.8	501	3	US-09-733-524-1
9	2070.5	86.7	454	4	US-10-120-319-8
10	2070.5	86.7	454	4	US-10-189-977-8
11	2070.5	86.7	454	4	US-10-392-098-8
12	2064.5	86.5	454	3	US-09-733-524-18
13	2058.5	86.2	476	3	US-09-733-524-15
14	2058.5	86.2	476	4	US-10-120-319-5
15	2058.5	86.2	476	4	US-10-189-977-5
16	2058.5	86.2	476	4	US-10-392-098-5
17	2050.5	85.9	479	3	US-09-733-524-17
18	2040.5	85.4	485	5	US-10-764-212-6
19	2036	85.3	486	4	US-10-120-319-2
20	2036	85.3	486	4	US-10-189-977-2
21	2036	85.3	486	4	US-10-392-098-2
22	2036	85.3	486	5	US-10-764-212-2
23	2026	84.8	485	3	US-09-733-524-2
24	1972.5	82.6	425	4	US-10-120-319-6
25	1972.5	82.6	425	4	US-10-189-977-6
26	1972.5	82.6	425	4	US-10-392-098-6
27	1972.5	82.6	425	5	US-10-764-212-12

28	1957	82.0	424	3	US-09-733-524-16	Sequence 16, Appl
29	1894.5	79.3	432	5	US-10-764-212-4	Sequence 4, Appl
30	1884	78.9	436	4	US-10-335-977-8559	Sequence 8559, Ap
31	1861	77.9	440	4	US-10-120-319-3	Sequence 3, Appl
32	1861	77.9	440	4	US-10-189-977-3	Sequence 3, Appl
33	1861	77.9	440	4	US-10-392-098-3	Sequence 3, Appl
34	1861	77.9	440	5	US-10-764-212-18	Sequence 18, Appl
35	1846	77.3	440	3	US-09-733-524-3	Sequence 3, Appl
36	1835	76.8	421	4	US-10-335-977-8558	Sequence 8558, Ap
37	1815	76.0	391	5	US-10-764-212-66	Sequence 66, Appl
38	1812.5	75.9	456	5	US-10-764-212-20	Sequence 20, Appl
39	1812	75.9	372	4	US-10-120-319-13	Sequence 13, Appl
40	1812	75.9	372	4	US-10-189-977-13	Sequence 13, Appl
41	1804	75.5	377	5	US-10-764-212-68	Sequence 68, Appl
42	1192	49.9	277	5	US-10-764-212-8	Sequence 8, Appl
43	1191	49.9	246	5	US-10-764-212-75	Sequence 75, Appl
44	1187	49.7	246	5	US-10-764-212-74	Sequence 74, Appl
45	1183.5	49.6	247	5	US-10-764-212-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-10-764-212-16
; Sequence 16, Application US/10764212
; Publication No. US20050164338A1

GENERAL INFORMATION:

; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 FutB fucosyltransferase

Description

Query Match	100.0%	Score 2388;	DB 5;	Length 446;
Best Local Similarity	100.0%	Pred. No. 9.2e-191;	Indels 0;	Gaps 0;
Matches 446;	Conservative 0;	Mismatches 0;		
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Db	1	MFQPLLDAYVESASIEKMASPPPLKIAVANWGDDEEIKFVKSVLYTFISQRYTIALH	60	
Qy	61	QNPNEFSDLVFNPNLGSARKILSYQNAKRVFTTGENEVNFNLFDAIGAIDELDFDRDYL	120	
Db	61	QNPNEFSDLVFNPNLGSARKILSYQNAKRVFTTGENEVNFNLFDAIGAIDELDFDRDYL	120	
Qy	121	RMPLYDYDRLLHKAESVNDTTSYKLDKNSLYTLKKPSHQFKNHNLCAVNDSDPLKR	180	
Db	121	RMPLYDYDRLLHKAESVNDTTSYKLDKNSLYTLKKPSHQFKNHNLCAVNDSDPLKR	180	
Qy	181	GVVSFVSNANAPMENAFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCFEN	240	
Db	181	GVVSFVSNANAPMENAFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFLSQYKFNLCFEN	240	
Qy	241	SGQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKEFVNVDHFNFDRAIDYIKYLH	300	
Db	241	SGQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKEFVNVDHFNFDRAIDYIKYLH	300	
Qy	301	PNAYLDMLYENPLNADGKAYFYQDLSFKKILAFKLTILENDTYIHKSTSFNWCCLDE	360	


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; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-10-392-098-1

Query Match      87.4%; Score 2086; DB 4; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.7e-165;
Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

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DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTITLH 60
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DB 61 QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNPNFLDYAIGFDELDFNDRL 120
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DB 121 RMPLYYDRLHKAESVNDTTPYKLDKNSLYALKPKSHCFKPKHNPILCAVNDSDPLKR 180
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DB 181 GYVSFVASNANAPRNAPIRNAFYDALNSIEPVTGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
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DB 241 TOGYGVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFKNFDEAIDYIKYLH 300
QY 301 PNAYLDMLYENPLNLDGKAYFQDLSPFKILAFKTLILENDTIYHKSSTSPWMECDLDE 360
DB 301 KNAYLDMLYENPLNLDGKAYFYQNLSPFKILAFKTLILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLVRVYDDLVRVYDDLVRVYDDLVRV 392
DB 359 PLVTIDDLRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRIN 418
QY 393 YDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 437
DB 419 YDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 463

RESULT 5
US-10-392-098-7
; Sequence 7, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-10-120-319-7

Query Match      86.8%; Score 2073; DB 4; Length 478;
Best Local Similarity 84.5%; Pred. No. 2.1e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTITLH 60
QY 61 QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNPNFLDYAIGFDELDFRDRL 120
```

```
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-10-392-098-7

Query Match      87.1%; Score 2079; DB 4; Length 478;
Best Local Similarity 84.7%; Pred. No. 6.7e-165;
Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTITLH 60
QY 61 QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNPNFLDYAIGFDELDFRDRL 120
DB 61 QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNPNFLDYAIGFDELDFNDRL 120
QY 121 RMPLYYDRLHKAESVNDTTPYKLDKNSLYTLKXPSHQFKNHNPILCAVNDSDPLKR 180
DB 121 RMPLYYDRLHKAESVNDTTPYKLDKNSLYALKPKSHCFKPKHNPILCAVNDSDPLKR 180
QY 181 GYVSFVASNANAPRNAPIRNAFYDALNSIEPVTGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GYVSFVASNANAPRNAPIRNAFYDALNSIEPVTGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SQGYGVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFNNFDEAIDYIKYLH 300
DB 241 TOGYGVTEKILDAYFSHTIPIYWGSPSAKDFNPKFVNVHDFKNFDEAIDYIKYLH 300
QY 301 PNAYLDMLYENPLNLDGKAYFQDLSPFKILAFKTLILENDTIYHKSSTSPWMECDLDE 360
DB 301 KNAYLDMLYENPLNLDGKAYFYQNLSPFKILAFKTLILENDTIYH--DNPFIFCRDLNE 358
QY 361 PLASIDDLRV-----NYDDLVRVYDDLVRVYDDLVRVYDDLVRV 392
DB 359 PLVTIDDLRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRIN 418
QY 393 YDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 437
DB 419 YDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRV 463

RESULT 6
US-10-120-319-7
; Sequence 7, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-10-120-319-7

Query Match      86.8%; Score 2073; DB 4; Length 478;
Best Local Similarity 84.5%; Pred. No. 2.1e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTIALH 60
DB 1 MFQPLLDAYVESASIEKMAKSPPLKIAVANWGWDEEIKFKKSVLYFIFSQRYTITLH 60
QY 61 QNPNEFSDLVFNPLGSAKILSYQNAKRVFTYTGNEVPNPNFLDYAIGFDELDFRDRL 120
```

Db	61	QNPNEFSDLVFGNPLGSARKILSYQNAKRVFTTGENESPENLFDYAI	GFDELD	FNDRL	120			
Qy	121	RMPLYDRLHHKAESVNDTTPSYKLKNSLYTLKPKSHQFKEHHPNLCAV	VNDESD	PLKR	180			
Db	121	RMPLYDRLHHKAESVNDTTPSYKLKNSLYTLKPKSHQFKEHHPNLCAV	VNDESD	PLKR	180			
Qy	181	GVVSFVASNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFL	SOYKFNLC	CFEN	240			
Db	181	GFASFVASNPNAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFL	SOYKFNLC	CFEN	240			
Qy	241	SOQGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKFQFVNVDHFN	PDPAIDYIKYL	HTH	300			
Db	241	TOQGYVTEKIIDAYFSHTTPIYWGSPSVAKDNPKFQFVNVDHFN	PDPAIDYIKYL	HTH	300			
Qy	301	PNAYLDMLYENPLNALDGKAYFYODLSFKKTLAPFKKLTILENDT	TYVHKSSST	SFMWEC	360			
Db	301	KNAYLDMLYENPLNLTDGKAYFYQNLSPKKLIDFKKLTILENDT	TYVH--DN	PFICRDLNE	358			
Qy	361	PLASIDDLRV-----	NYDDL	RVNYDDL	RVNYDDL	RVN	392	
Db	359	PLVTIDDLRVNYDDL	RVNYDDL	RVNYDDL	RVNYDDL	RVNYDDL	RVN	418
Qy	393	YDDL	RVNYDDL	RVNYERLLQNASLLELSQNTSFKI	RYAKQKPI	437		
Db	419	YDDL	RVNYDDL	RVNYERLLSKATP	LLSQNTTSKI	RYAKQKSL	463	

RESULT 7

US-10-189-977-7

; Sequence 7, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge. Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-7

Query Match

Best Local Similarity

Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2

Qy	1	MFQPLLDAYVESASIEKMASKSPPLKLANVWGDDEIKPKKSVLYFIF	SQRYTIALH	60		
Db	1	MFQPLLDAYVESASIEKMASKSPPLKLANVWGDDEIKPKKSVLYFIF	SQRYTIALH	60		
Qy	61	QNPNEFSDLVFSNPLGSARKILSYQNAKRVFTTGENEVPENFNL	FDYAI	GFDELD	FDRYL	120
Db	61	QNPNEFSDLVFGNPLGSARKILSYQNAKRVFTTGENESPENLFDYAI	GFDELD	FNDRL	120	
Qy	121	RMPLYDRLHHKAESVNDTTPSYKLKNSLYTLKPKSHQFKEHHPNLCAV	VNDESD	PLKR	180	
Db	121	RMPLYDRLHHKAESVNDTTPSYKLKNSLYTLKPKSHQFKEHHPNLCAV	VNDESD	PLKR	180	
Qy	181	GVVSFVASNANAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFL	SOYKFNLC	CFEN	240	
Db	181	GFASFVASNPNAPRNAPFYDALNSIEPTVGGSGVKNLTGYNVKNKSEFL	SOYKFNLC	CFEN	240	
Qy	241	SOQGYVTEKILDAYFSHTTPIYWGSPSVAKDNPKFQFVNVDHFN	PDPAIDYIKYL	HTH	300	


```
QY 407 YERLLQNASPLLELSONTSFKIYRKAYQKPI 437
|||||:|||||:|||||:|||||:
Db 419 YERLLSKATPLLELSONTSKIYRKAYQKSL 449

RESULT 9
US-10-120-319-8
; Sequence 8, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-8

Query Match 86.7%; Score 2070.5; DB 4; Length 454;
Best Local Similarity 86.5%; Pred. No. 3.2e-164;
Matches 384; Conservative 27; Mismatches 24; Indels 9; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWGDEEIKEPKKSVLYFISQRYTIALH 60
|||||:|||||:|||||:|||||:
Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWGDEEIKEPKKSVLYFISQRYTIALH 60

QY 61 QNPNEFSLVFSNPLGSAKILSYQNAKRVFTYTGNEVPNPNLFDYAGFDELDFRDYL 120
|||||:|||||:|||||:|||||:
Db 61 RNPDKPADIVFCGNPLGSAKILSYQNTKRIFTYGENESPNNLFDYAGFDELDFRDYL 120

QY 121 RMPLYYDLRHHAESVNDTTPYKLGNSLYTLKKPSHCFCENHPNLCALINNESDPLKR 180
|||||:|||||:|||||:|||||:
Db 121 RMPLYYDLRHHAESVNDTTPYKLGNSLYTLKKPSHCFCENHPNLCALINNESDPLKR 180

QY 181 GVVSFVASNANAPRNAFYDALNSIEPTVGGSVKNTLGVNVKNKSEFLSQYKFNLCFEN 240
|||||:|||||:|||||:|||||:
Db 181 GPASFVASNANAPRNAFYDALNSIEPTVGGAVKNTLGYKVGKSEFLSQYKFNLCFEN 240

QY 241 SOGYGVVTEKILDAYFSHTPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLH 300
|||||:|||||:|||||:|||||:
Db 241 SOGYGVVTEKILDAYFSHTPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLH 300

QY 301 PNAYLDMLYENPLNADGKAFYQDLSPFKKILAFKTIENDTIYHKSSTSFNWECDLDE 360
|||||:|||||:|||||:|||||:
Db 301 PNAYLDMLYENPLNADGKAFYQDLSPFKKILAFKTIENDTIYH--NNPFIYFDLNE 358

QY 361 PLASIT-----DGLRVNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYL 413
|||||:|||||:|||||:|||||:
Db 359 PLVSDINLRINYDNLVRNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYL 418

QY 414 ASPLLELSONTSFKIYRKAYQKPI 437
|||||:|||||:|||||:
Db 419 ASPLLELSONTSFKIYRKAYQKSL 442

RESULT 11
US-10-392-098-8
; Sequence 8, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
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Db 1 MFQPLLDAFIESASIEKMWKSPPPPLKIAVANWGWDEIEIKFKKSVLYFISQRYAITL 60
Qy 60 HQNPNEFSDLVFNSPLGSAKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 119
Db 61 HQNPNESSDLVFNPLGAARKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 120
Qy 120 LRMPLYYDLRHHKASVNDTTSYKLNKNSLYTLKKPSHQFKENHPNLCAVNDSDPLK 179
Db 121 LRMPLYYAHLYEAEVLNDTTPAYKLNKNSLYALKKPSHHFKENHPNLCAVNDSDLLK 180
Qy 180 RGVSVFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 239
Db 181 RGFASFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 240
Qy 240 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 299
Db 241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 300
Qy 300 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYHKSSTSPFWMECDLD 359
Db 359 EPLISIDDLRVNVDLVRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 418
Qy 418 NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 437
Db 437 NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 464
RESULT 14
US-10-120-319-5
; Sequence 5, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-5
Query Match 86.2%; Score 2058.5; DB 4; Length 476;
Best Local Similarity 84.5%; Pred. No. 3.4e-163;
Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;
Qy 1 MFQPLLDAYVESASIEKMWKSPPPPLKIAVANWGWDEIEIKFKKSVLYFISQRYAITL 59
Db 1 MFQPLLDAYVESASIEKMWKSPPPPLKIAVANWGWDEIEIKFKKSVLYFISQRYAITL 60
Qy 60 HQNPNEFSDLVFNSPLGSAKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 119
Db 61 HQNPNESSDLVFNPLGAARKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 120
Qy 120 LRMPLYYDLRHHKASVNDTTSYKLNKNSLYTLKKPSHQFKENHPNLCAVNDSDPLK 179
Db 121 LRMPLYYAHLYEAEVLNDTTPAYKLNKNSLYALKKPSHHFKENHPNLCAVNDSDLLK 180
Qy 180 RGVSVFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 239
Db 181 RGFASFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 240
Qy 240 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 299
Db 241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 300
Qy 300 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYHKSSTSPFWMECDLD 359
Db 359 EPLISIDDLRVNVDLVRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 418
Qy 418 NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 437
Db 437 NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 464

Qy 240 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 299
Db 241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 300
Qy 300 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYHKSSTSPFWMECDLD 359
Db 301 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYH--NNPFIYRDLH 358
Qy 360 EPLASI-----DDLVRVNYDDLRVNYDDLRVNYDDLRV 391
Db 359 EPLISIDDLRVNVDLVRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 418
Qy 392 NYDDLRVNYDDLRVNYERLQNASPLLELSONTSFKIYKAYQKPI 437
Db 419 NYDDLRVNYDDLRVNYERLQNASPLLELSONTSFKIYKAYQKSL 464
RESULT 15
US-10-189-977-5
; Sequence 5, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-5
Query Match 86.2%; Score 2058.5; DB 4; Length 476;
Best Local Similarity 84.5%; Pred. No. 3.4e-163;
Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;
Qy 1 MFQPLLDAYVESASIEKMWKSPPPPLKIAVANWGWDEIEIKFKKSVLYFISQRYAITL 59
Db 1 MFQPLLDAYVESASIEKMWKSPPPPLKIAVANWGWDEIEIKFKKSVLYFISQRYAITL 60
Qy 60 HQNPNEFSDLVFNSPLGSAKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 119
Db 61 HQNPNESSDLVFNPLGAARKILSYONAKRVFTYTGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 120
Qy 120 LRMPLYYDLRHHKASVNDTTSYKLNKNSLYTLKKPSHQFKENHPNLCAVNDSDPLK 179
Db 121 LRMPLYYAHLYEAEVLNDTTPAYKLNKNSLYALKKPSHHFKENHPNLCAVNDSDLLK 180
Qy 180 RGVSVFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 239
Db 181 RGFASFVASNANAPRNAFYDALNSIEPTVGGGSVKNLTGYNVKNKSEFLSQYKFNLCFE 240
Qy 240 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 299
Db 241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSAKDNPKFVNVDHFNFDNFIYKYLHT 300
Qy 300 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYHKSSTSPFWMECDLD 359
Db 301 HPNAYLDMLYENPLNADGKAYFYQDLSFKKILAFPKTILENDTIYH--NNPFIYRDLH 358
Qy 360 EPLASI-----DDLVRVNYDDLRVNYDDLRVNYDDLRV 391
Db 359 EPLISIDDLRVNVDLVRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 418

QY 392 NYDDLRYNDDLRVNYERLLQNASPLLELSONTSFKIYRKAYQKPI 437
Db 419 NYDDLRYNDDLRVNYERLLQNASPLLELSONTSFKIYRKAYQKSL 464

Search completed: August 11, 2006, 19:53:05
Job time : 109.675 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:47:49 ; Search time 16.9493 Seconds
(without alignments)
1771.230 Million cell updates/sec

Title: US-10-764-212-16
Perfect score: 2388
Sequence: 1 MFQPLLDVYASIEKMAS.....KIYKAYQKIPKPPYCAP 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148.5	6.2	302	US-10-953-349-5129	Sequence 5129, Ap
2	148.5	6.2	323	US-10-953-349-5128	Sequence 5128, Ap
3	148.5	6.2	338	US-10-953-349-5127	Sequence 5127, Ap
4	137.5	5.8	246	US-10-449-902-44967	Sequence 44967, A
5	137.5	5.7	406	US-11-197-712-284	Sequence 284, App
6	127.5	5.3	513	US-10-449-902-52598	Sequence 52598, A
7	124.5	5.2	2133	US-10-537-642-9	Sequence 9, Appli
8	122	5.1	336	US-11-293-697-4748	Sequence 4748, Ap
9	119.5	5.0	3029	US-10-537-642-10	Sequence 10, Appl
10	118.5	5.0	1781	US-10-537-642-24	Sequence 24, Appl
11	110	4.6	2404	US-10-537-642-3	Sequence 3, Appli
12	109	4.6	615	US-10-449-902-48384	Sequence 48384, A
13	107	4.5	2024	US-10-537-642-21	Sequence 21, Appl
14	106	4.4	954	US-10-537-642-8	Sequence 8, Appli
15	106	4.4	1464	US-10-537-642-27	Sequence 27, Appl
16	105	4.4	852	US-11-293-582-25	Sequence 25, Appl
17	105	4.4	858	US-10-527-411-22	Sequence 22, Appl
18	105	4.4	1169	US-10-527-411-20	Sequence 20, Appl
19	104	4.4	860	US-10-527-411-175	Sequence 175, App
20	104	4.4	866	US-10-527-411-94	Sequence 94, Appl
21	104	4.4	862	US-10-527-411-88	Sequence 88, Appl
22	104	4.4	867	US-10-527-411-96	Sequence 96, Appl
23	104	4.4	867	US-10-527-411-98	Sequence 98, Appl
24	104	4.4	870	US-10-527-411-92	Sequence 92, Appl
25	104	4.4	871	US-10-527-411-84	Sequence 84, Appl

26	104	4.4	871	6	US-10-527-411-86	Sequence 86, Appl
27	104	4.4	871	6	US-10-527-411-90	Sequence 90, Appl
28	103	4.3	862	6	US-10-527-411-171	Sequence 171, App
29	103	4.3	862	6	US-10-527-411-173	Sequence 173, App
30	103	4.3	866	6	US-10-527-411-104	Sequence 104, App
31	103	4.3	1420	6	US-10-527-411-110	Sequence 110, App
32	102.5	4.3	742	6	US-10-471-571A-1894	Sequence 1894, Ap
33	102.5	4.3	867	6	US-10-527-411-80	Sequence 80, Appl
34	102.5	4.3	888	6	US-10-527-411-112	Sequence 112, Appl
35	102	4.3	126	6	US-10-126-915-4	Sequence 4, Appli
36	101.5	4.3	1575	6	US-10-505-928-257	Sequence 257, App
37	100.5	4.2	397	6	US-10-471-571A-5110	Sequence 5110, Ap
38	100.5	4.2	855	6	US-10-521-401A-11	Sequence 11, Appl
39	100.5	4.2	1066	6	US-10-521-401A-13	Sequence 13, Appl
40	100.5	4.2	1067	6	US-10-521-401A-14	Sequence 14, Appl
41	100	4.2	1791	6	US-10-537-642-18	Sequence 18, Appl
42	98.5	4.1	416	7	US-11-056-355B-75786	Sequence 75786, A
43	98.5	4.1	423	7	US-11-056-355B-75785	Sequence 75785, A
44	98.5	4.1	953	6	US-10-471-571A-3528	Sequence 3528, Ap
45	98.5	4.1	1434	7	US-11-192-046-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-953-349-5129
; Sequence 5129, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5129
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5129

Query Match 6.2%; Score 148.5; DB 6; Length 302;
Best Local Similarity 25.8%; Pred. No. 0.00015;
.Matches 51; Conservative 34; Mismatches 78; Indels 35; Gaps 7;
QY 179 KRGVSVFVASNANAPMRNAPFYDAL-----NSIEPVTGGGSKVNTLGYNVKNKSBFLSOYK 233
Db 9 ERAIAAFISNGA--RNFLQLALEAMKTNIKIDSYGGCHNRDG--KYDKVEALKRYK 64
QY 234 FNLCPENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNP--KEFVNVDHFNFNDEAI 291
Db 65 FSLAFTNTEEDYVTEKPFQSLVAGSPVVGVPNI--EEFAPASDSFLHIKTMEDVEPVA 123
QY 292 DYIKYLHFNAYLMDL-----YENPLNALDGKAYFYQDLSFKKILAPFKTILE----- 340
Db 124 KMKYLAANPAAYNTQLRWKYGSPDSFKALVDMAAVHSSCLCIFLATRVREOEESPN 183
QY 341 -----NDTIYH 346
Db 184 FKKRCPKCSRGGSDTVYH 201

RESULT 2
US-10-953-349-5128
; Sequence 5128, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY

```
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PUBLICATION NO. US20060107345A1
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5128
; LENGTH: 323
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-5128

Query Match      6.2%; Score 148.5; DB 6; Length 323;
Best Local Similarity 25.8%; Pred. No. 0.00017;
Matches 51; Conservative 34; Mismatches 78; Indels 35; Gaps 7;

Qy 179 KRGVVSFVSNANAPMNAFYDAL-----NSIEPVTTGGSGVNTLGYNVKNSBFLSQYK 233
Db 30 ERAIAAFAFISNCGA--RNFRQLQALEALMKTNIKIDSYGGCHNRDQ--KVDKVEALKRYK 85
Qy 234 FNLCFENSQGVYVTEKILDAYFSHTIPIYWGSPSVAKDNF--KEFVNVHDFNPFDEAI 291
Db 86 FSLAFENTNEEDYVTEKPFQSLVAGSPVVPVGPNNI--EEFAPASDSFLHIXTMEDEVPA 144
Qy 292 DYIKYLTHPNAYLDML---YENPLNALDGKAYFYQDLSFKKILAFFKFTILE----- 340
Db 145 KRMKYLAAAPAAYNQTLRWKYEGSDSFKALVDMAAVHSSCELCIFLATRVREQEESPN 204
Qy 341 -----NDTIYH 346
Db 205 FKRPCKCSRGSGSDTVYH 222

RESULT 3
US-10-953-349-5127
; Sequence 5127, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5127
; LENGTH: 338
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-5127

Query Match      6.2%; Score 148.5; DB 6; Length 338;
Best Local Similarity 25.8%; Pred. No. 0.00018;
Matches 51; Conservative 34; Mismatches 78; Indels 35; Gaps 7;

Qy 179 KRGVVSFVSNANAPMNAFYDAL-----NSIEPVTTGGSGVNTLGYNVKNSBFLSQYK 233
Db 45 ERAIAAFAFISNCGA--RNFRQLQALEALMKTNIKIDSYGGCHNRDQ--KVDKVEALKRYK 100
Qy 234 FNLCFENSQGVYVTEKILDAYFSHTIPIYWGSPSVAKDNF--KEFVNVHDFNPFDEAI 291
Db 101 FSLAFENTNEEDYVTEKPFQSLVAGSPVVPVGPNNI--EEFAPASDSFLHIXTMEDEVPA 159
Qy 292 DYIKYLTHPNAYLDML---YENPLNALDGKAYFYQDLSFKKILAFFKFTILE----- 340
Db 160 KRMKYLAAAPAAYNQTLRWKYEGSDSFKALVDMAAVHSSCELCIFLATRVREQEESPN 219
Qy 341 -----NDTIYH 346
Db 220 FKRPCKCSRGSGSDTVYH 237

RESULT 4
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US-10-449-902-44967
; Sequence 44967, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 44967
; LENGTH: 246
; TYPE: PRP
; ORGANISM: Oryza sativa
; US-10-449-902-44967

Query Match      5.8%; Score 137.5; DB 6; Length 246;
Best Local Similarity 23.9%; Pred. No. 0.00089;
Matches 50; Conservative 34; Mismatches 94; Indels 31; Gaps 6;

Qy 120 LRMPLYYD-RLHKAESVNDTTPSYKLKDNLSYTLK-KPSHQFKENHNLCAVNDSDP 177
Db 4 LPLRVYLDLEAARKPTGPEDFIGYHAKDDQVTVYAGKSFHTSRSYH-----VSTEK-- 55
Qy 178 LKRGVVSFVSNANAPMNAF-----NAFYDANLSIEPTVCGGSKVNTLGYNVKN 224
Db 56 -RNDALTYWSSRCLPHRDVKVAKDFLSLVPHHSFGKCLNNDGDPKALSMYVPCVSTNDNG 114
Qy 225 KSEF-----LSQYKPNLCFENSQGVYVTEKILDAYFSHTIPIYWGSPSVAKDNFNPKE 277
Db 115 KPHWDHLHCAMSHYKFFVALIENTKTESYVTEKLFYALEAGSVPIYFGAPVNDFFPPNS 174
Qy 278 FVNVHDFNPFDEAIDYIKYLTHPNAYLD 306
Db 175 IIDASKFSSRLASLYVKAANDPVAYAE 203

RESULT 5
US-11-197-712-284
; Sequence 284, Application US/11197712
; Publication No. US20060130160A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US 4 CIP
; CURRENT APPLICATION NUMBER: US/11/197,712
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/876,997
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pn
; SEQ ID NO 284
; LENGTH: 406
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
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LOCATION: -31...-1
US-11-197-712-284

Query Match 5.7%; Score 137; DB 7; Length 406;
Best Local Similarity 24.5%; Pred. No. 0.0021;
Matches 80; Conservative 43; Mismatches 142; Indels 62; Gaps 12;
QY 35 GDEEKEKPKSVLYPIFGORVTHALQNP-----NBFSDLVFNSPLGS 77
DB 75 GKFEKEKSSLOCHTQWEEAPTHLSFLKKEGLTNRKEKWLDSYPIMLWSPLTG 134
QY 78 AKILSYQNAKRVYVTEGNEVNFNLFYAIGFDELDFRDRYLRMPYYDRHLHKAESVYN 137
DB 135 ETGRGCGGACACFTT-INRTYLHHMTKAFLYGTDFNIDSLPLP-----RKAHDHWAFF 189
QY 138 DTTSP---YKLKNSLYTLKPSHOF-KENHPNLCAVNDSDPLKR----- 180
DB 190 HEESPKNKYLFHKPVITLTNYATATFSRSHLPLTTQYLESIEVLKSLRYLPLQSKNKL 249
QY 191 ---GVVSFVASNANAPMENAFY--DALNSIEPTVGGSGVKH-TLGYNNVKNK----- 226
DB 250 RKRLAPLVVQSCDPPSDRSYVRELMTYIEVDSYGECLRNKDLPOQLKNPASHMDAGF 309
QY 227 -EFLSQYKFNLCFENSQSGYGVYTEKILDAYFSHTIPIYWGSPSVAKDFNP--KEFVNVDH 283
DB 310 YRIIAQYKFIILAFENAVCDDYITEKFWRLKLGVPVYVYGSIT-DWLPSNKSAILVSE 368
QY 284 FNNFDEAIDYIKLHTHPNAVLDMLYE 310
DB 369 FSHPRELASYIRRLDSD-----DRLYE 390

RESULT 6

US-10-449-902-52598
Sequence 52598, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205V1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 52598
LENGTH: 513
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-52598

Query Match 5.3%; Score 127.5; DB 6; Length 513;
Best Local Similarity 26.1%; Pred. No. 0.017;
Matches 40; Conservative 33; Mismatches 55; Indels 25; Gaps 6;
QY 190 ANAPMRNAYDALNSIEPV-----TGGSGVNTLGYNNVKNKSEFLSQYKFNLCFENSQGY 244
DB 230 SNGCARNFRLQALEMLESILDKIDSYSGCHRNHDG--KVDVETLTKYKFSLAFENSNEE 287
QY 245 GYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKE--FVNVDHFNFPDEAIDYIKLHTHPN 302
DB 288 DYVTEKFFQSIVTGAIPVVGAPNI-QSFSGEGAILHIKELDDVPSIAKTMKHTASNOE 346
QY 303 AYLDML---YENPLNALDGKAYFYQDLSFKKIL 332
DB 347 AFNQLRWKYDGPSPD-----SFKALI 367

RESULT 7

US-10-537-642-9
Sequence 9, Application US/10537642
Publication No. US20060165719A1
GENERAL INFORMATION:
APPLICANT: Epimmune, Inc.
APPLICANT: The United States of America as Represented by the
APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Doolan, Denise L.
APPLICANT: Carucci, Daniel J.
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: Patent in version 3.2
SEQ ID NO 9
LENGTH: 2133
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-537-642-9

Query Match 5.2%; Score 124.5; DB 6; Length 2133;
Best Local Similarity 22.0%; Pred. No. 0.25;
Matches 83; Conservative 45; Mismatches 145; Indels 105; Gaps 19;

QY 104 PDYAIGF-----DELDFRDYRLMPLYDDRLHKAESVNDTSPYKLNKNSLYTLKK 155
DB 18 FHLKLGFFVCYKXNDKYSFKNKILQK-----NTILFFKKKKFMYLRKK 63
QY 156 PSHQPKENHPNLCAVVNDESPLK-----RGVVSFVASNANAPMRNAYDALNSIEP 207
DB 64 KKKKKKILIIQIYKNNKYFKYNSNLEGNQGFNKKPEKNKT-KGNVYTDHTNQ--- 119
QY 208 VTGGSGVNTLGYNNVKNKSEFLSQYKFN-----LCFENSQGYGVYTEKILDAYSHT 259
DB 120 -----NAKSKI-YNYDMDDDSYNNVNNNNVFRISFLILANNEFFGY----- 160
QY 260 IPIYWGSPSVAKDFNPKEFVNVDHFNFPDEAIDYIKLHTHPNAYLDMLYENPLNALDGK 319
DB 161 -PLQFVCEGSRNHEHYPDVHGDNIKYKCDNKNKCDNKNY-DKCDNKNKCDN 218
QY 320 AVFYQDLSFKILAPFKTILENDTIYHKSSSTPMWECDDLEPLASIDDLRVN-YDDLVRN 378
DB 219 KYDTCD-----DNKYD-----TCD-DNKYDTCDDNKNKYDDDKYD 253
QY 379 -YDDLVRN-YDDLVRN-YDDLVRN-YDDLVRN-YDDLVRN-YDDLVRN-YDDLVRN-YDDLVRN 426
DB 254 TCDDNKNKYDDDKYKYYDDDKYKYYDDDKYKYYDDDKYKYYDDDKYKYYDDDKYKYYDDDKYK 313
QY 427 KIYKAYQKPIKNPYPC 444
DB 314 CVINKIYKYPK-----YC 327

RESULT 8

US-11-293-697-4748
Sequence 4748, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28

Db 680 NCNVEKYINNSFINNKSSINIKDDVVYNGMNDNHHNNNNNTLCNTSLDLCNNSS 739
QY 243 GYGYVTEKILDYFHSHTPIYWGSPSAVD-----FNPKEFVNVDHFNPFDEAIDYK 295
Db 740 ESKQEAUCLAKNDTHDI-----IKNSVNMKPSLYMPPINNNNNNNNDTSTNNVQ 794
QY 296 YLHTHPNAYL-----DMLYENPLNALDOKAYFYQDLS---PKKILAFPKTILENTIYH 346
Db 795 FINNTYNDYFYDEKDEQHPFYDNKKNKIKFRNIRIIRIIEKEDEQEHTEKNNTIEN 854
QY 347 KSSTSPMWECDL-----RVNYDDLRVNYDDLRVNYDDLRVNYDDLR- 404
Db 855 KVNVEIMYSKEITNMNINRSDEYITNNMNDNMMNTLYPWKENFKNVDMNLNIYK 914
QY 370 VNYDDL-----RVNYDDLRVNYDDLRVNYDDLRVNYDDLR- 404
Db 915 INKDYLDYDVIKNDVISPYKDPNIIMDRIN-DDNNINMNDNLLTYEQMNNHNNKK 973
QY 405 ---VNYERLLQNASPLLELSQNTSPKIYRK 431
Db 974 WNVFNNSIILEKNEKITNSKKQNYKIHQR 1003
RESULT 11
US-10-537-642-3
; Sequence 3, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2404
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-3
Query Match 4.6%; Score 110; DB 6; Length 2404;
Best Local Similarity 22.6%; Pred. No. 4.7;
Matches 95; Conservative 61; Mismatches 159; Indels 106; Gaps 24;
QY 36 DEIKPEKSVLYPIFSQRYTIALHQNPNE---FSDLVFNPLGSAKILSYQ----- 85
Db 268 DVENIEKKKNKYEYIKKNIYDSYNDIREMSLCFYLLNLLNRDKICVFFNLESEKN 327
QY 86 --NAKRVFTYGENEVPNFNLFDYA-IGFDELDFRDRYLRMPLYDRLHH-KAESVNDTTS 141
Db 328 TINAFSINTGVNPEAMQLNDKASLLFDN-----VYEEKENSREEDINDKVS 376
QY 142 PY--KLKD-----NSLY-----TLKKPSHOFKGNHPLNLCVAVNDESPLKRGVVSFVASNAN 191
Db 377 KQGCNLNDSNSVLYINIQNIKDYLKEDNKYNDVBNQMLNRFMNVNKEENVDLKN 436
QY 192 APMENAFDALNSLEPTVGGSVKNTLGVNKNKSEFLSQYK-FNLCPENSQGYGVVTEK 250
Db 437 MALHIFFYKIIDEETHVHH-----MNKKE-----YKYFFLVKMLFLHNYLLEK 480
QY 251 ILDAYFSHTPIYWGSPSAVDKPNKPFVN--VHDFNNFDEAIDYK-YLHTHPNAYLDM 307
Db 481 M-----NMLNLCIDNLEFNFIYKIIKEAVHTHICDYLD- 514

QY 308 LYENPLNALDGKAY--FYQDLSFKKILAFK-KTILEN--DTIYHK-SSTSPMWECDLDEP 361
Db 515 VYNFLKLLQRYEYSNLIKSRNSDLNFFNSSIIQNLINFLCQKISQDVFIIEYD-DMP 573
QY 362 LASIDDLRVNYDD-LRVNYD-----DLRVNYDDLRV-----NYDDLVRVNYDDL 404
Db 574 FEDKDNFEMSYKNILKEKYECFLPFDLSFLRDDINMLCKRGDATDNDNEDNI-INSNDR 632
QY 405 V 405
Db 633 L 633
RESULT 12
US-10-449-902-48384
; Sequence 48384, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48384
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48384
Query Match 4.6%; Score 109; DB 6; Length 615;
Best Local Similarity 19.8%; Pred. No. 0.75;
Matches 92; Conservative 73; Mismatches 174; Indels 126; Gaps 23;
QY 37 ERIKEPKSVLYPIFSQRYTIALHQNPNEPSDLVFNPLGSAKILSYQNAK-----RVFY 92
Db 144 EBITQAESQLVVYQDSAQY---LSPYPKVQTTLSIRLPGGRVSEYTKYPNTKLAESLKY 200
QY 93 TGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYDRLHHKAESVNDTTSYKLDNSLYT 152
Db 201 GYEDLPFES-----YSPMVHY-----ENNPFVAKEVIRE 233
QY 153 LKKPSH-----QPKENHPNLC-----AVNDESPLKRGVVSFVASNANAPMR--N 196
Db 234 I-EISHGNVQITE-HYNIAHGGAKLKGFESRIDYQSRPYIRGVSSPRHLIARLPRAHS 291
QY 197 AFY-DALNSIE-----PVTGGSVKNTLGVNKNKSEFLSQYKFN 236
Db 292 IYRDEIGNISTSHLWSDSKKTQLEVPFPPLGGWQTTFTIGYGLP-----LQDFVF-- 344
QY 237 CPENSQGYGVVTEKILDYFHSHTPIYWGSPSAVDKPNKPFVN---HDFNNFDEAIDY 293
Db 345 ---NSDGKFLN-----ITFGSP-VEEILIEKLIKVLVLPESKIDISVFP 387
QY 294 -----IKYLHT-----HPNAVLDMLYENPLNALDGKAYF-YQDLSFKK-----ILAFK 336
Db 388 PTKQGEVYKSHLDISGRPVVLEKLDVIPLEHNLVYQVYVFNNSILLRPPMMLITGFFL 447
QY 337 -----TILENTIYHKSTSPMWECDLDEPLASIDDLRVNYDDLRVNYDDLRVNYDDL 390
Db 448 LFMACIVYTRMTDSISKNSPSYLAQVQWDEVOIIQIQIAIFNOCLAADKLETSLHEL 507
QY 391 VNYD--DLRVNYDDLRVNYERLLQNASPLLELSQNT--SPKIYRK 431

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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:30:38 ; Search time 116.066 Seconds
(without alignments)
1733.289 Million cell updates/sec

Title: US-10-764-212-18
Perfect score: 2362
Sequence: 1 MFQPLLDAFIESASIKKMP.....YHKSLPLRAIRRWVKLGL 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2362	100.0	440	9	AEB70147 Helicobac
2	2347	99.4	440	5	ABG30883
3	2007.5	85.0	485	8	ADJ77814 Helicobac
4	2007.5	85.0	485	8	ADJ27349 Alpha-1.3
5	2007.5	85.0	485	9	AEB70135 Helicobac
6	2006.5	84.9	454	5	ABG30887
7	1999	84.6	486	8	ADJ77810 Helicobac
8	1999	84.6	486	9	ABG30882
9	1999	84.6	486	9	AEB70131 Helicobac
10	1984.5	84.0	485	5	ABG30884 H. pylori
11	1982.5	83.9	476	5	ABG30882
12	1978	83.7	464	2	AAW86008
13	1970.5	83.4	432	8	ADJ77812 Helicobac
14	1970.5	83.4	432	8	ADJ27347 Alpha-1.3
15	1970.5	83.4	432	9	AEB70133 Helicobac
16	1970	83.4	501	5	ABG30881
17	1960.5	83.0	479	5	ABG30886
18	1879.5	79.6	425	8	ADJ77820 Helicobac
19	1879.5	79.6	425	8	ADJ27355 Alpha-1.3
20	1879.5	79.6	425	9	AEB70141 Helicobac
21	1869	79.1	424	5	ABG30885
22	1861	78.8	446	9	AEB70145 Helicobac
23	1842.5	78.0	418	5	ABU52257

ALIGNMENTS

RESULT 1
AEB70147
ID AEB70147 standard; protein; 440 AA.
XX
AC AEB70147;
XX
DT 06-OCT-2005 (first entry)
XX
DE Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 18.
XX
KW Fucosyltransferase; protein production; enzyme.
XX
OS Helicobacter pylori; strain 802.
XX
FH Key Location/Qualifiers
FT Misc-difference 112
ET /note= "Encoded by TTT"
XX
FN US2005164338-A1.
XX
PD 28-JUL-2005.
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX (UYAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KP, Bezila DJ;
DR WPI; 2005-521417/53.
XX N-PSDB; AEB70146.
XX
CC New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Claim 1; SEQ ID NO 18; 97pp; English.
XX
CC The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucoseyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

Aeb70197 H. pylori
Aeb70195 H. pylori
Aeb70149 Helicobac
Adj77816 Helicobac
Adj27351 Alpha-1,3
Aeb70137 Helicobac
Aeb70199 H. pylori
Aeb70204 H. pylori
Aeb70203 H. pylori
Aeb70193 H. pylori
Aeb70201 H. pylori
Aeb70202 H. pylori
Aeb70206 Helicobac
Aeb70205 H. pylori
Aeb70211 Helicobac
Aeb70154 H. pylori
Aeb70212 Helicobac
Abu51720 Helicobac
Abu51151 Helicobac
Abu51509 Helicobac
Abu51153 Helicobac
Aeb70177 H. pylori

Db	421	YHKSPLLRARRRWYKGL 440	QY	178	GFASFVASHNPAPKRNAPFYDALNSIEBPVTGGGSSVONTLGHVKNKNEFLSOYKFNLCFEN	237
			Db	181	GFASFVASHNPAPKRNAPFYDALNSIEBPVIGGSSVONTLGNINKSEFLSOYKFNLCFEN	240
RESULT 3			QY	238	SQGYGVVTEKIIDAYESHPTIPIYWGSPSAKDFNPKSFVNVDKFNDFEADIDYVRYLHTH	297
ADJ77814			Db	241	SQGYGVVTEKIIDAYESHPTIPIYWGSPSAQDFNPKSFVNVDKFNDFEADIDHRYLHTH	300
AC	ADJ77814;		QY	298	FNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFEKTILENDTIYHNNPFVFFYRDLNEPL	357
DT	06-MAY-2004 (first entry)		Db	301	FNAYLDMLYENPLNTLDGKAYFYQNLSPFKILDFEKTILENDTIYHNDPFIYRDLNEPL	360
XX			QY	358	VSIDDLRADYNNMLRADYNNMLRADYNNMLRADYD-----	396
DE	Helicobacter pylori strain 1218 FutB protein SeqID 6.		Db	361	ISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYD	420
KW	FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;		QY	397	-----RLQNRSPLLELSQNTTFKIYKAYHKSPLLRARRRW	435
KW	fucose; N-acetylglucosamine; glycoconjugate; enzyme.		Db	421	DLRVNCDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYKAYOKSUPLLRAARKLI	480
XX	Helicobacter pylori.		QY	436	KXGL 440	
FN	WO2004009838-A2.		Db	481	KXGL 485	
XX	29-JAN-2004.					
XX	23-JUL-2003; 2003WO-US023057.		RESULT 4			
XX	23-JUL-2002; 2002US-0398156P.		ADJ27349			
PR	08-NOV-2002; 2002US-0424894P.		ID	ADJ27349	standard; protein; 485 AA.	
XX	(NEOS-) NEOSE TECHNOLOGIES INC.		XX	ADJ27349;		
PA	Johnson KF, Bezila DJ;		XX	20-MAY-2004 (first entry)		
PI	WPI; 2004-123401/12.		DT	Alpha-1,3/4-fucosyltransferase.		
DR	N-PSDB; ADJ77813.		XX	alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;		
XX	New isolated polynucleotide encoding fucosyltransferase protein, useful		KW	fucosyl; fucose.		
PT	for synthesizing oligosaccharide moiety on a protein or lipid that is		XX	Helicobacter pylori; strain 1218 FutB.		
PT	unglycosylated in its native form or for synthesizing glycolipids.		OS			
XX	Claim 16; SEQ ID NO 6; 72pp; English.		XX	WO2004009793-A2.		
PS	This invention relates to novel isolated polynucleotides and the encoded		XX	29-JAN-2004.		
XX	polypeptides thereof, which are related to the fucosyltransferase enzymes		XX	23-JUL-2003; 2003WO-US023155.		
CC	(FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it		XX	23-JUL-2002; 2002US-0398156P.		
CC	refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to		PR	08-NOV-2002; 2002US-0424894P.		
CC	chemically synthesise glycoproteins and glycolipids with the desired		XX	(NEOS-) NEOSE TECHNOLOGIES INC.		
CC	oligosaccharide moieties (i.e. by transfer of a fucose residue to N-		PA	Johnson KF, Bezila DJ;		
CC	acetylglucosamine), such that they are useful in the preparation of		XX	WPI; 2004-132958/13.		
CC	glycoconjugates. The present invention describes how bacterial		DR	N-PSDB; ADJ27348.		
CC	fucosyltransferase is unaffected by the sialylation status of the acceptor		XX	Producing fucosylated glycoprotein, by contacting recombinant		
CC	sugar, as opposed to the mammalian homologue, and furthermore,		PT	fucosyltransferase protein with mixture comprising donor substrate and		
CC	bacterially expressed enzymes offer a large cost saving relative to		PT	acceptor substrate on glycoprotein.		
CC	mammalian expression systems. This polypeptide sequence is an H. pylori		XX	Claim 1; Fig 3; 84pp; English.		
CC	strain 1218 FutB protein sequence of the invention.		XX	This sequence represents an alpha-1,3/4-fucosyltransferase protein which		
XX	Sequence 485 AA;		CC	was used in the method of the invention for producing a fucosylated		
Query Match	85.0%; Score 2007.5; DB 8; Length 485;		CC	glycoprotein. The method involves contacting a recombinant		
Best Local Similarity	78.1%; Pred. No. 1.3e-175;		CC	fucosyltransferase protein with a mixture comprising a donor substrate		
Matches 379; Conservative 34; Mismatches 27; Indels 45; Gaps 3;			CC	which comprises a fucosyl residue, and an acceptor substrate on a		
1 MFQPLLDAFIESASIKQM-PLSYPLKIAVANWGG--ABEPKGSAMFILLSQRTITLH 57			CC	glycoprotein, under conditions such that the fucosyltransferase protein		
1 MFQPLLDAFIESASIEKITSKPPPLKIAVANWGGDEBVEBPKKNILFYILLSQHYTILH 60			CC	catalyzes the transfer of the fucose residue from a donor substrate to		
58 QNPNEPSDLVFGSPIGSARKILSVQNAKRVFTGENSPNLFDAIYGFDELDRDYL 117			CC	the acceptor substrate on the glycoprotein. The method is useful for		
61 QNPNEPSDLVFGSPIGSARKILSVQNAKRVFTGENSPNLFDAIYGFDELDRDYL 120			CC	producing fucosylated glycoprotein.		
118 RMPLYYDLRHHKASVNDTTPYIKPDSLYTLKKPSSHFKPKPHLCVAVNDESDPLKR 177			XX	Sequence 485 AA;		
121 RMPLYYDLRHHKASVNDTTPYIKPDSLYTLKKPSSHFKPKPHLCVAVNDESDPLKR 180						

PD 28-JUL-2005.
XX 22-JAN-2004; 2004US-00764212.
XX 22-JAN-2004; 2004US-00764212.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA (UYAL-) UNIV ALBERTA.
XX Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
DR N-PSDB; AEB70130.
XX New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX Example 1; SEQ ID NO 2; 97pp; English.
XX The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.
XX
SQ Sequence 486 AA;
Query Match 84.6%; Score 1999; DB 9; Length 486;
Best Local Similarity 77.6%; Pred. No. 8.2e-175;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;
Qy 1 MFQPLLDAPFESASIKKM-PLSYPLPKIAVANWGG--AEPFKGAMFILLSQRTITLH 57
Db 1 MFQPLLDAYIESAIEKITSPPPKIAVANWGDVEBVEFKNLYFIILLSQHYTITLH 60
Qy 58 QNPNEPSDLVPGSPIGARKILSYONKTRVFAGNEVPNPNLDPYATGPFELDLDRYL 117
Db 61 QNPNEPSDLVPGSPIGARKILSYONAKRVFTYGENSPNPNLDPYATGPFELDLDRYL 120
Qy 118 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKPPSHHFKKHPHLCVAVNDESDPLKR 177
Db 121 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKPPSHHFKKHPHLCVAVNDESDPLKR 180
Qy 178 GFASFVSNPNAPKRNAPYDALNSIEPVTGGSVKNTLGYKVGKNRFLSQYKFNLCFEN 237
Db 181 GFASFVSNPNAPKRNAPYDVLNLSIEPIVGGSVKNTLGYNKKSEFLSQYKFNLCFEN 240
Qy 238 SQGYGYTEKILIDAYFSTHPIIYGGSPVAVDFNPKSFVNVHDFKPFDEADIVRYLH 297
Db 241 SQGYGYTEKILIDAYFSTHPIIYGGSPVAVDFNPKSFVNVHDFKPFDEADIVRYLH 300
Qy 298 PNAVLDMLYENPLNLQKAYFYODLSPKKILDPFKTILENDTIYHNNPFFVYRDLNPL 357
Db 301 PNAVLDMLYENPLNLQKAYFYQNLSPKKILDPFKTILENDTIYHNDNPFYRDLNPL 360
Qy 358 VSI-----DDLRADYNNLRADY 374
Db 361 ISIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNY 420
Qy 375 NNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNN 434
Db 421 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNY 480
Qy 435 VKKLGL 440
Db 481 IKKLGL 486

RESULT 10
ABG30882
ID ABG30882 standard; protein; 485 AA.

XX ABG30882;
XX 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX H. pylori alpa1,3 fucosyltransferase #2.
KW Enzyme; fucT; alpa1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
XX sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX Helicobacter pylori; strain 1182.
XX US2002068347-A1.
PD 06-JUN-2002.
XX 07-DEC-2000; 2000US-00733524.
XX 05-JUN-1998; 98US-00092315.
XX (UYAL-) UNIV ALBERTA.
XX Taylor DE, Ge Z;
XX WPI; 2002-582480/62.
XX Purified transmembrane segment-free alpa1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.
XX Claim 6; Fig 6; 37pp; English.
XX The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpa1,3- fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpa1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpa1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpa1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpa1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alpa1,3
CC fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX Sequence 485 AA;
Query Match 84.0%; Score 1984.5; DB 5; Length 485;
Best Local Similarity 77.6%; Pred. No. 1.8e-173;
Matches 377; Conservative 34; Mismatches 28; Indels 47; Gaps 4;

QY 1 MFQPLDAPFESASIKKM-PLSYPPPLKIAVANWGG--AEEPKSAMFYTLISQRYITILH 57
 DB 1 MFQPLDAPFESASIKKM-PLSYPPPLKIAVANWGG--AEEPKSAMFYTLISQRYITILH 60
 QY 58 QNPNEPSDLVFGSPIGSARILSYQNTKRVFYAGENEVNFNFDYAIGFDELDRDYL 117
 DB 61 QNPNEPSDLVFGSPIGSARILSYQNTKRVFYAGENEVNFNFDYAIGFDELDRDYL 120
 QY 118 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKPKHPLCAVNNDESPLKR 177
 DB 121 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKPKHPLCAVNNDESPLKR 180
 QY 178 GFASFVASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEPFLSOYKFNLCFEN 237
 DB 181 GFASFVASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEPFLSOYKFNLCFEN 240
 QY 238 SQQGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNPDEAIDVYVYLTH 297
 DB 241 SQQGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNPDEAIDVYVYLTH 300
 QY 298 PNAYLDMLENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYRDLNEPL 357
 DB 301 PNAYLDMLENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYRDLNEPL 360
 QY 358 VSI-----DDLRADYNNLRADY 374
 DB 361 ISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 420
 QY 375 NLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLR 434
 DB 421 DDURVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 479
 QY 435 VKKGL 440
 DB 480 IKKGL 485

RESULT 11
 ABG30884
 ID ABG30884 standard; protein; 476 AA.
 AC ABG30884;
 XX
 XX 29-AUG-2003 (revised)
 DT 21-OCT-2002 (first entry)
 XX
 XX H. pylori alpha1,3 fucosyltransferase #4.
 DE
 XX Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
 KW slx; Helicobacter pylori infection; malignant cell; mammalian tumour.
 XX
 OS Helicobacter pylori; strain 26695A.
 XX
 PN US2002068347-A1.
 XX
 XX 06-JUN-2002.
 PD
 XX 07-DEC-2000; 2000US-00733524.
 XX
 XX 05-JUN-1998; 98US-00092315.
 PR
 XX (UVAL-) UNIV ALBERTA.
 XX
 XX Taylor DE, Ge Z;
 XX WPI; 2002-582480/62.
 DR
 XX Purified transmembrane segment-free alpha1,3-fucosyltransferase
 PT polypeptide useful for producing fucosylated oligosaccharides.
 XX
 XX Example 3; Fig 6; 37pp; English.
 PS
 XX

CC The invention relates a purified transmembrane segment-free alpha 1,3-
 CC fucosyltransferase polypeptide, having a repeat of the sequence: X1-X2-
 CC Leu-Arg-X3-X4-Tyr, where X1, X2 and X4 is Asp or Asn; and X3 is
 CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
 CC (including its complement or fragment), a vector containing the nucleic
 CC acid, a host cell containing nucleic acid or vector, an antibody which
 CC selectively binds to the protein and a gene expression system for
 CC producing transmembrane segment-free alpha1,3-fucosyltransferase,
 CC comprising a host cell modified with the nucleic acid or its
 CC enzymatically active portion. The protein and cells are useful for
 CC producing fucosylated oligosaccharides, such as Lex, Ley or slx, by
 CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
 CC and purifying the produced oligosaccharides, or by culturing the cell,
 CC contacting the host cell with a substrate, to produce oligosaccharides
 CC and purifying the obtained oligosaccharides. The nucleic acid is useful
 CC as a probe for detecting the nucleic acid, by contacting a sample with a
 CC nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
 CC polynucleotide, and detecting hybridisation of the probe; or by
 CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
 CC host cell is useful for producing a transmembrane segment-free alpha1,3-
 CC fucosyltransferase-fusion protein, by growing the host cell containing a
 CC vector operably linked to a polynucleotide encoding a desired polypeptide
 CC or peptide under conditions which allow expression and secretion of the
 CC fusion protein and isolating the fusion protein. The antibody is useful
 CC for detecting the protein in a sample. The presence of the protein in the
 CC sample is indicative of infection by Helicobacter pylori or the presence
 CC of malignant cells. The antibody is also useful for diagnosing disorders
 CC and monitoring disease, and for inhibiting abnormal alpha1,3-
 CC fucosyltransferase gene product activity. The nucleic acid is useful as
 CC part of ribozyme and/or triple helix sequences and for alpha1,3-
 CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
 CC the protein or cell are useful in the development of assays to detect
 CC mammalian tumours. The present sequence represents an H. pylori alpha1,3
 CC fucosyltransferase encoded by the fucT gene. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 476 AA;

Query Match 83.9%; Score 1982.5; DB 5; Length 476;
 Best Local Similarity 78.6%; Pred. No. 2.6e-173;
 Matches 374; Conservative 30; Mismatches 33; Indels 39; Gaps 3;
 QY 1 MFQPLDAPFESASIKKMPLSY--PPLKIAVANWGGAE--EPPKISAMFYTLISQRYITIL 56
 DB 1 MFQPLDAPFESASIKKMPLSY--PPLKIAVANWGGAE--EPPKISAMFYTLISQRYITIL 60
 QY 57 HQNPNEPSDLVFGSPIGSARILSYQNTKRVFYAGENEVNFNFDYAIGFDELDRDY 116
 DB 61 HQNPNEPSDLVFGSPIGSARILSYQNTKRVFYAGENEVNFNFDYAIGFDELDRDY 120
 QY 117 LRMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKPKHPLCAVNNDESPLK 176
 DB 121 LRMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKPKHPLCAVNNDESPLK 180
 QY 177 RGFASFVASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEPFLSOYKFNLCF 236
 DB 181 RGFASFVASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEPFLSOYKFNLCF 240
 QY 237 NSQGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNPDEAIDVYRDL 296
 DB 241 NSQGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNPDEAIDVYRDL 300
 QY 297 HPNAYLDMLENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYRDLNEP 356
 DB 301 HPNAYLDMLENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYRDLNEP 360
 QY 357 LVSI-----DDLRADYNNLRADYNNLRADY 381
 DB 361 LISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 420
 QY 382 NLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLR 437
 DB 421 DDURVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 476

RESULT 12

AAW86008

ID AAW86008 standard; protein; 464 AA.

XX AC AAW86008;

XX DT 17-OCT-2003 (revised)

XX DT 29-MAR-1999 (first entry)

XX DE Helicobacter pylori

XX DE Helicobacter pylori alpha-1,3-fucosyltransferase.

KW Alpha-1,3-fucosyltransferase; fuct gene; Lewis X; Lewis Y;

KW sialyl Lewis X; tumour associated antigen; cancer; infection;

KW mucosal disease; diagnosis; fucosylated oligosaccharide.

XX Helicobacter pylori; strain NCTC 11639.

XX FH Key

XX FH Location/Qualifiers

XX FT Modified-site 96..99

XX FT /note= "Asn is N-glycosylated"

XX FT Modified-site 137..139

XX FT /note= "Asn is N-glycosylated"

XX FT Modified-site 332..334

XX FT /note= "Asn is N-glycosylated"

XX FT Modified-site 341..343

XX FT /note= "Asn is N-glycosylated"

XX FT Peptide 364..370

XX FT /note= "peptide repeat"

XX FT Peptide 371..377

XX FT /note= "peptide repeat"

XX FT Peptide 378..384

XX FT /note= "peptide repeat"

XX FT Peptide 385..391

XX FT /note= "peptide repeat"

XX FT Peptide 392..398

XX FT /note= "peptide repeat"

XX FT Peptide 399..405

XX FT /note= "peptide repeat"

XX FT Peptide 406..412

XX FT /note= "peptide repeat"

XX FT Peptide 413..419

XX FT /note= "peptide repeat"

XX FT Modified-site 435..437

XX FT /note= "Asn is N-glycosylated"

XX PN W0985630-A2.

XX PD 10-DEC-1998.

XX PF 05-JUN-1998; 98WO-CA000564.

XX PR 06-JUN-1997; 97US-0048857P.

XX XX (UTAL-) UNIV ALBERTA.

XX PA Taylor DE, Ge Z;

XX PI WPI; 1999-059913/05.

XX DR N-PSDB; AAW80321.

XX DR New isolated alpha-1,3-fucosyltransferase gene - obtained from

XX FT Helicobacter pylori, used to develop products for the diagnosis and

XX FT treatment of intestinal mucosal diseases, e.g. tumours.

XX PS Claim 6; Fig 2; 51pp; English.

XX CC This is the amino acid sequence of the novel alpha-1,3-

XX CC fucosyltransferase of Helicobacter pylori NCTC 11639, as deduced from the

XX CC newly isolated fuct gene (see AAW80321). The enzyme is characterised by 8

XX CC C-terminal heptad repeats and by the lack of a transmembrane domain. The

XX CC absence of a transmembrane domain allows the enzyme to be readily

CC released from recombinant host cells. The enzyme can be used in the
 CC production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
 CC sialyl Lewis X, which are structurally similar to certain tumour
 CC associated antigens found in mammals. These glycoconjugates also have
 CC research and diagnosis utility in the development of assays to detect
 CC mammalian tumours. The enzyme can also be used to raise specific
 CC antibodies. Inhibition of abnormal fuct gene product activity can be used
 CC for the treatment of intestinal mucosal disease. (Updated on 17-OCT-2003
 CC to standardise OS field)

XX SQ Sequence 464 AA;

Query Match 83.7%; Score 1978; DB 2; Length 464;

Best Local Similarity 80.6%; Pred. No. 6.6e-173;

Matches 374; Conservative 32; Mismatches 34; Indels 24; Gaps 3;

QY 1 MFQPLLDAFIESASIKOM-PLSYPLPKIAVANWGGAE--BFKKSAMYPILSQRYTITLH 57

DB 1 MFQPLLDAYVESASIEKMASKSPPLPKIAVANWGGDEIEKEFKNSVLYFILSQRYTITLH 60

QY 58 QNPNEPSDLVFGSPICGAARKILSYQNTKRVFYAGENEVPNFNFYDVAIGDELDRDYL 117

DB 61 QNPNEPSDLVFGNPLGSAARKILSYQNAKRVFYTGENSEPNFNFYDVAIGDELDFNDYL 120

QY 118 RMPLYDYDLRHKAESVNDTTAPYKIKPDSLYTLKPSHHFKKHPHLCAVVNDESDPLKR 177

DB 121 RMPLYDYDLRHKAESVNDTTAPYKLDNSLYALKKPSHCFKKHPNLCAVVNDESDPLKR 180

QY 178 GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSKVNTLGYKVGKNEFLSQYKFNLCFEN 237

DB 181 GFASFVASNPNAPIRNAFYDALNSIEPVTGGGSRNTLGYNVKNKNEFLRQYKFNLCFEN 240

QY 238 SOGYGVYTEKIIDAYESHTEPIYWGSPSAKDNPKSFVNVHDFKPFDEALDYVRYLHTH 297

DB 241 TQGYGVYTEKIIDAYESHTEPIYWGSPSAKDNPKSFVNVHDFKPFDEALDYIKYLHTH 300

QY 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVYRDLNEPL 357

DB 301 KNAYLDMLYENPLNTLDGKAYFYQNLSPFKILAFFKTILENDTIYHDNPFIFCEDLNEPL 360

QY 358 VSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNN 396

DB 361 VTIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYE 420

QY 397 RLLQNRSPLELSQNTTFKIIYKAYHKSPLRLRAIRRWVKKGL 440

DB 421 RLLSKATPLLELSQNTTSKIYRKAYOKSLPLRAIRRWVKKGL 464

RESULT 13

ADJ77812

ID ADJ77812 standard; protein; 432 AA.

XX AC ADJ77812;

XX DT 06-MAY-2004 (first entry)

XX DE Helicobacter pylori strain 1111 FutA protein SeqID 4.

XX KW FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;

XX KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.

XX OS Helicobacter pylori.

XX XX WO2004009838-A2.

XX XX 29-JAN-2004.

XX XX 23-JUL-2003; 2003WO-US023057.

XX XX 23-JUL-2002; 2002US-0398156P.

XX XX 08-NOV-2002; 2002US-0424894P.

XX XX


```
PA (NEOS-) NEOSE TECHNOLOGIES INC.
PI Johnson KF, Bezila DJ;
XX WPI; 2004-123401/12.
DR N-PSDB; ADJ77811.
XX
PT New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
XX unglycosylated in its native form or for synthesizing glycolipids.
XX
PS Claim 16; SEQ ID NO 4; 72pp; English.
XX
CC This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesize glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar, as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 1111 FutA protein sequence of the invention.
XX
SQ Sequence 432 AA;

Query Match 83.4%; Score 1970.5; DB 8; Length 432;
Best Local Similarity 82.5%; Pred. No. 2.9e-172;
Matches 362; Conservative 39; Mismatches 29; Indels 9; Gaps 2;

QY 1 MFQPLLDAFIESASIKKMPPLKIAVANWGGAE--EFKKSAMYPILSQRYTITLHQ 58
DB 1 MFQPLLDAFIESAPLKKWPLNPLKIAVANWGGDEEIKFKKSVLYFILSQHYTITLHR 60
QY 59 NPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVFNPNLFDYATGDFDLDRYL 118
DB 61 NPDKPADIVFGNPLGSAARKILSYQNAKRVFYTGNEVFNPNLFDYATGDFDLDRYL 120
QY 119 MPLYYDLRLHKAESVNDTAPYKIKPDSLYTLKKPSHHFKEKHPHLCVAVNDESDPLKRG 178
DB 121 MPLYYAYLHYKAEVLNDTTPYKIQPDSLYALKKPSHHFKEKHPHLCVAVNDESDPLKRG 180
QY 179 FASVFNAPNAPKRNAPFYDALNSIEPTVGGSGVKNLTGYKGVGNKNEFLSQYKFNLCFENS 238
DB 181 FASVFNAPNAPRNAPFYDALNSIEPTVGGSGVKNLTGYKGVGNKNEFLSQYKFNLCFENS 240
QY 239 QGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNKDFDAIDYRYLHTHP 298
DB 241 QGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNKDFDAIDYRYLHTHP 300
QY 299 NAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFEFTKILENDTIYHNNPFVYFDLNEPLV 358
DB 301 NAYLDHMYENPLNTLDGKAYFYQNLSEFKKILDFEFTKILENDTIYHNNPFVYFDLNEPSV 360
QY 359 SIDDRLADYNRLADYNRLADYNRLADYNRLADYNRLADYNRLADYNRLADYNRLADYN 418
DB 361 SID-----GLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYR 413

RESULT 14
ADJ27347
ID ADJ27347 standard; protein; 432 AA.
XX
AC ADJ27347;
XX
PT 20-MAY-2004 (first entry)
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: August 11, 2006, 19:37:09 ; Search time 20.6557 Seconds
(without alignments)
2049.570 Million cell updates/sec
Title: US-10-764-212-18
Perfect score: 2362
Sequence: 1 MFQPLLDAPFIESASIKKMP...YHKSLPLRAIRRWVKLGL 440
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2039	86.3	436	G71862	alpha-(1,3)-fucosyltransferase
2	1982.5	83.9	476	C64601	alpha-(1,3)-fucosyltransferase
3	1960.5	83.0	454	B71914	alpha-(1,3)-fucosyltransferase
4	1879.5	79.6	425	C64567	hypothetical protein
5	187	7.9	346	T44327	hypothetical protein
6	160.5	6.8	513	F86533	probable fucosyltransferase
7	147.5	6.2	183	C97832	alpha-(1,3)-fucosyltransferase
8	137.5	5.8	433	A57596	alpha-(1,3)-fucosyltransferase
9	134.5	5.7	451	T23491	hypothetical protein
10	129.5	5.5	324	A1879	hypothetical protein
11	128.5	5.4	400	JC4591	alpha-1,3 fucosyltransferase
12	127.5	5.4	789	G90587	lipoprotein (import)
13	126.5	5.4	3973	B71612	hypothetical protein
14	124.5	5.3	405	B36340	alpha-(1,3)-fucosyltransferase
15	124	5.2	393	H96742	hypothetical protein
16	124	5.2	525	T28306	ORF MSV145
17	124	5.2	631	T45950	hypothetical protein
18	123.5	5.2	1272	H82926	conserved hypothetical protein
19	123	5.2	361	A36669	3-alpha-galactosyltransferase
20	121.5	5.1	3394	T18501	hypothetical protein
21	120.5	5.1	810	A19782	virB4 protein precursor
22	120	5.1	414	T15270	hypothetical protein
23	119.5	5.1	605	A1917	hypothetical protein
24	119	5.0	608	T28301	ORF MSV140
25	118.5	5.0	689	AC1408	transcription anti-sense
26	118.5	5.0	689	AC1784	transcription anti-sense
27	117.5	5.0	365	S55498	alpha(1,3/4)-fucosyltransferase
28	117.5	5.0	403	F90283	hypothetical protein
29	117	5.0	1127	T28317	ORF MSV156

RESULT 1
G71862
alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436
A:Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000036D2; GB:AE001528; GB:AE001439; NID: A:Experimental source: strain J99

ALIGNMENTS

30	116.5	4.9	1004	2	A71617	SERA antigen/papain type I restriction
31	116	4.9	1104	2	B75221	hypothetical protein
32	115.5	4.9	2500	2	G71609	hypothetical protein
33	115	4.9	817	2	C64695	type I restriction
34	114.5	4.8	1084	2	C82931	hypothetical protein
35	114	4.8	2380	2	E71604	hypothetical protein
36	114	4.8	5005	2	F82884	hypothetical protein
37	113.5	4.8	359	2	A45156	alpha-(1,3)-fucosyltransferase
38	113.5	4.8	364	2	I39048	alpha-(1,3)-fucosyltransferase
39	113.5	4.8	624	2	A84150	hypothetical protein
40	112.5	4.8	1146	2	E70204	hypothetical protein
41	112	4.7	836	2	T18460	hypothetical protein
42	112	4.7	1338	2	T18416	hypothetical protein
43	111.5	4.7	2206	2	G71611	hypothetical protein
44	110.5	4.7	1346	2	G71613	hypothetical protein
45	110.5	4.7	1639	2	S05603	major merozoite surface protein

Query Match 86.3%; Score 2039; DB 2; Length 436;
Best Local Similarity 86.5%; Pred. No. 8.1e-135;
Matches 384; Conservative 25; Mismatches 23; Indels 12; Gaps 3;

QY	1	MFQPLLDAPFIESASIKKMP	SY-----PPLKIAVANWGGAEFFKKSAMFYILSQRYTITL	56
DB	1	MFQPLLDAPFIESPTIKK-KITFKSPPLKIAVANWGGAEFFKKS	TLXLFILSQRYTITL	59
QY	57	HQNPNEPSDLVFGSPITGAARKILSYQNTKRVFVAGENEVPNFN	LDYVAIGFDELDRDY	116
DB	60	HQNPNEPSDLVFGSPITGAARKILSYQNTKRVFVAGENEVPNFN	LDYVAIGFDELDRDY	119
QY	117	LRMPLYRLAHKAESVNDTTAPYKIPDSLYTLKPKSHHFKHPLCAV	NDESPLK	176
DB	120	LRMPLYRLAHKAESVNDTTAPYKIPDSLYTLKPKSHHFKHPLCAV	NDESPLK	179
QY	177	RGFASVSNPNAPKRNAPYDALNSIEPTGGSGVNTLGKVGKNKNE	FLSQKFNLCPE	236
DB	180	RGFASVSNPNAPKRNAPYDALNSIEPTGGSGVNTLGKVGKNKNE	FLSQKFNLCPE	239
QY	237	NSQGYGYTEKILIDAFSHTIPIYWGSPSVAKDNPKSFVNVDKFN	EDAIYVRLHT	296
DB	240	NTQGYGYTEKILIDAFSHTIPIYWGSPSVAKDNPKSFVNVDKFN	EDAIYVRLHT	299
QY	297	HPNAVLDMLYENPLNTLQKAYFYQDLSPFKILDFFKTLLENDTI	YHNPNFVYRDLNEP	356
DB	300	HPNAVLDMLYENPLNTLQKAYFYQDLSPFKILDFFKTLLENDTI	YHNPNFVYRDLNEP	359
QY	357	LVSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRAD	YNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRAD	416
DB	360	LVAIDD-----LRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYD	RLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYD	412
QY	417	YHAKTHKSLPLRAIRRWVKLGL		440

[illegible]

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RESULT 7
C97832
alpha-(1,3)-fucosyltransferase homolog RC1059 [imported] - Rickettsia conorii (strain Ma
C|Species: Rickettsia conorii
C|Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C|Accession: C97832
R|Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A|Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A|Reference number: A97700; MUID:21442074; PMID:11557893
A|Accession: C97832
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-183 <KUR>
A|Cross-references: UNIPROT:Q9ZGR3; UNIPARC:UPI00000CBFA7; GB:AE006914; PIDN:AAL03597.1;
C|Genetics:
A|Gene: RC1059

Query Match          6.2%; Score 147.5; DB 2; Length 183;
Best Local Similarity 28.6%; Pred. No. 0.0025;
Matches 44; Conservative 22; Mismatches 69; Indels 19; Gaps 5;

Qy 173 DPLKRGASFWAS-----NENAPKRNAPFDALNSIEPVTGGSGVKNTLGYKVGNK--N 223
      ||| ||| : ||| : : : : : ||| : : : : :
Db 13 NPNTYFACFLVNSGISEPENGDCIARNRPFHKLISLYKKVSGSKYLNTSTIIPEKTR 72
      ||| ||| : ||| : : : : : ||| : : : : :
Qy 224 EFLSQYKFNLCFENSQGYGYVTEKIIIDAYFSHTIP-IYWGSPSVAKDNPKFSFVNVDPK 282

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Db 73 EWLSCKCFVAFENKTSSEGYVAKPFAYLAGAVHIIYADKSVIKDQVNSVIFAKDYS 132
Qy 283 NFDEAIDYV-----RYLTHPNAYLDMLYEN 308
Db 133 E-EDLYNYIISVGKDKDEKYYKIYNNKIYPALENN 165

RESULT 8
A57596
alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.1) - mouse
N;Alternate names: ELAM-1 ligand fucosyltransferase homolog
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57596
R;Gersten, K.M.; Natsuka, S.; Trincheria, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.; Je
J. Biol. Chem. 270, 25047-25056, 1995
A;Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific exp
erases.
A;Reference number: A57596; MUID:96027607; PMID:7559635
A;Accession: A57596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <GER>
A;Cross-references: UNIPROT:Q11127; UNIPARC:UPI000004039; GB:U33457; NID:g1039426; PIDN
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: Glycosyltransferase; hexosyltransferase

Query Match 5.8%; Score 137.5; DB 2; Length 433;
Best Local Similarity 22.4%; Pred. No. 0.04;
Matches 80; Conservative 48; Mismatches 130; Indels 99; Gaps 17;

Qy 6 LDATFESASIKMPLSYV-PLK-IATANWNGGAEFFKKSAMFYLSQRYTTLHQNPNEP 63
Db 67 LTTFCWQGLPPLWASPAPQLVGLVLMW---BPFGRGGY-----PKSP 109
Qy 64 SLDVFGSPIGAARKILSVQNTKRVFYAGENEVNFN-----LFDYAIGFDELDRDY 116
Db 110 PDCSLRFNISGRLL-----TDRAAY-GEAQLVHFHRDLVKELHWDPPPGARERTDKA 163
Qy 117 LRMPLYYDR-----LHKHKAESVNDTAPY 140
Db 164 LVLAFFDDQGANVLTGKALETVGSRPGQVWVWVNFSPSHPTCLRLGLAKDLFNWTLSY 223
Qy 141 KIKPD-----SLYTLKKPSHHFKKHPLCAVNDSDPLKRGFASVFNAPNAPK-RN 193
Db 224 RTDSDVFPVYGFYLSRSDPTQPSGLGQLAR-----KRGIVAWVWVSNWNEHQARV 274
Qy 194 AFYDALNSIEPV-----TGGSVNTLGYKGNKNEFLSQYKFNLCFNSQGYGVVTEKI 248
Db 275 RYHQLSRHVSVDVFGRTGPRPVPAIGLL-----HTVARYKFLAFENSRHVDVITEKL 329
Qy 249 -IDAFVSHHTIPIYWGSPSA--KDFNPK-SPVNVHDFKNFDEAIDYRYLTHPNAY 301
Db 330 WRNAFLAGVPLVGL-PDRANYERFVPRGAFIHVDVDFNAASLAAYLLFLDRNAVY 385

RESULT 9
T23491
hypoetical protein K08F8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23491
R;Smyle, R.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z19747
A;Accession: T23491
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-451 <WIL>
A;Cross-references: UNIPROT:Q21362; UNIPARC:UPI000015543A; EMBL:Z66497; PIDN:CAA91285.1;
A;Experimental source: clone K08F8
C;Genetics:

A;Gene: CESP:K08F8.3
A;Map position: 2
A;Introns: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2

Query Match 5.7%; Score 134.5; DB 2; Length 451;
Best Local Similarity 28.0%; Pred. No. 0.069;
Matches 60; Conservative 32; Mismatches 89; Indels 33; Gaps 9;

Qy 113 RDRYLRMPLYYDRLLHKAESVNDTTA--PYKIKPDSLYTLKKPSHHFKKHPLCAVVD 170
Db 207 RPDYINMTLGR-----HDTAGSPYG-----YTVKLGAKSRKTGQVVDANLVNG 251
Qy 171 ESDPLKRGFASVFNAPNAPKRNAPFYDALN---SIEPVTGGSVVNTLGYKVGKNNEFL- 226
Db 252 KA-----KGAANFVSHCQTNKREDFVKLQKHLQIDDIYGGCGPMKCARG---DSKCDTML 304
Qy 227 -SQYKFNLCFNSQGYGVVTEKIIDAFVSHHT-IPYWGSPSVAKDFNPKSFVNVHDFKNP 284
Db 305 DTDYHFVYTFENSICEDYVTEKLMKSGYQNTIPLVLRKLVPEFPVPPNPSFIAIDDFKSV 364
Qy 285 DEADYRYLTHPNAYLDMW---YENPLNTLDG 315
Db 365 KEMGDYLYLNMNNTAYMEYFEWHRDHYKVVFLDG 398

RESULT 10
AH1879
hypoetical protein alr0585 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1879
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saegawa, M.; Watanabe, A.; Iriouchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH1879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <KUR>
A;Cross-references: UNIPROT:Q8Y294; UNIPARC:UPI000000CDDCA; GB:BA000019; PIDN:BAB72543.1;
A;Experimental source: strain PCC 7120
C;Genetics:

Query Match 5.5%; Score 129.5; DB 2; Length 324;
Best Local Similarity 22.0%; Pred. No. 0.097;
Matches 58; Conservative 43; Mismatches 88; Indels 75; Gaps 11;

Qy 81 YONTKRVFYAGENEVNFNLFYDIAIGFDELDRDRLMPLYYDRLLHKAESVNDTAPY 140
Db 116 YQEAKK--YCG-----YISGPDPAKPDYMPAIWYH---NNSFRELNEMPVPE 159
Qy 141 KIKPDLYTLKKPSHHFKKHPLCAVNDSDPLKRGFASVFNAPNAPKRNAPFYDALN 200
Db 160 KVFPCSWIT-----SGISRTVNRRLKLFVLIQ 188
Qy 201 SIE-----PVTGGSVVNTLGYKVGKNNEFLSQYKFNLCFEN-SQGQYGVVTEKII 249
Db 189 ASEVKCDYVGRDLPIWA-----KSLG-ELGNKWMGMAPYYNLSIENYDNDWYSEKLW 242
Qy 250 DAYFVSHHTIPIYWGSPSAKDFNPKSFVNVHDFKNFDEAIDYRYLTHPNAYL---DMLY 306
Db 243 DALLAWCLPIYGGPAADKLLPPGSLRPLPSLD--EKGIAYIQEVATPDPAWAAKDAIA 300
Qy 307 E-----NPLNTLDGKAYFYQDLS 324
Db 301 EARQLILHKLNLNLNLSEFVQTQFS 324

RESULT 11
JC4591

[illegible]

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: August 11, 2006, 19:30:58 ; Search time 154.754 Seconds
(without alignments)
2630.023 Million cell updates/sec
Title: US-10-764-212-18
Perfect score: 2362
Sequence: 1 MFQPLLDAPFISASIKKMP.....YHKSLPLRLAIRRWKLGKL 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2039	86.3	436	Q9ZKD7_HELPJ	Q9Zkd7 helicobacte
2	1982.5	83.9	476	Q25366_HELPY	Q25366 helicobacte
3	1975	83.6	478	Q30511_HELPY	Q30511 helicobacte
4	1960.5	83.0	454	Q9ZL13_HELPJ	Q9Zl13 helicobacte
5	1927.5	81.6	432	Q6ST35_HELPY	Q6st35 helicobacte
6	1879.5	79.6	425	Q25142_HELPY	Q25142 helicobacte
7	1769.5	74.9	462	Q918S4_HELPY	Q918s4 helicobacte
8	1509	63.9	333	Q32631_HELPY	Q32631 helicobacte
9	445	18.8	331	Q5L9S6_BACFN	Q5L9s6 bacteroides
10	431.5	18.3	359	Q7VFA1_HELPH	Q7Vfa1 helicobacte
11	327	13.8	287	Q21E19_9DEL	Q21e19 anaeromyxob
12	210	8.9	462	Q54PJ9_DICDI	Q54pj9 dictyosteli
13	195	8.3	665	Q54L56_DICDI	Q54l56 dictyosteli
14	193.5	8.2	417	Q6NAB_CIOIN	Q6nab clona intes
15	187	7.9	346	Q87156_VIBCH	Q87156 vibrio chol
16	184.5	7.8	389	Q54PH9_DICDI	Q54ph9 dictyosteli
17	180	7.6	777	Q54P60_DICDI	Q54p60 dictyosteli
18	177.5	7.5	219	Q3W50_MEDTR	Q3w50 medicago tr
19	177	7.5	600	Q5UQ63_MIMIV	Q5uq63 mimivirus.
20	175	7.4	510	Q9ST51_PHAOU	Q9st51 phaseolus a
21	173.5	7.3	348	Q6A1E3_CIOSA	Q6a1e3 clona savig
22	173	7.3	504	Q6Q5Y3_MEDTR	Q6q5y3 medicago tr
23	173	7.3	505	Q5DTC8_MEDSA	Q5dct8 medicago sa
24	173	7.3	506	Q5DTC9_MEDSA	Q5dct9 medicago sa
25	170	7.2	338	Q87135_VIBCH	Q87135 vibrio chol
26	169.5	7.2	349	Q6EVL1_XENTR	Q6evl1 xenopus tro
27	168.5	7.1	522	Q599J4_9ROSI	Q599j4 populus alb
28	167	7.1	338	Q34231_VIBCH	Q34231 vibrio chol
29	162	6.9	818	Q55FA8_DICDI	Q55fa8 dictyosteli
30	161	6.8	168	Q7P9H9_RICSI	Q7p9h9 rickettsia
31	160.5	6.8	513	FUT12_ARATH	Q9fx97 arabidopsais

32	160.5	6.8	513	2	Q5DTB2_ARATH	Q5dtb2 arabidopsais
33	160	6.8	377	2	Q70G69_IPONI	Q70g69 ipomoea nil
34	159	6.7	2226	2	O97225_PLAP7	O97225 plasmodium
35	158.5	6.7	533	2	O8L5D1_PHYPA	O8l5d1 physcomitre
36	157.5	6.7	413	2	O8VXF9_LYCES	O8vxf9 lycopersico
37	157	6.6	355	2	Q3SHR4_THIDA	Q3shr4 thioabacillu
38	157	6.6	463	2	Q54PK0_DICDI	Q54pk0 dictyosteli
39	155.5	6.6	436	2	Q2WBL9_MAIZE	Q2wb19 zea mays (m
40	155.5	6.6	533	2	Q6A2M3_PHYPA	Q6a2m3 physcomitre
41	155	6.6	501	2	Q4VMQ8_ARATH	Q4vmq8 arabidopsais
42	154	6.5	359	2	Q5F2N6_XENTR	Q5f2n6 xenopus tro
43	154	6.5	501	1	FUT11_ARATH	Q91jki arabidopsais
44	153	6.5	444	2	Q6A1D9_CIOSA	Q6a1d9 clona savig
45	151	6.4	349	2	Q3KQ28_XENLA	Q3kq28 xenopus lae

ALIGNMENTS

RESULT 1

Q9ZKD7_HELPJ

ID Q9ZKD7_HELPJ PRELIMINARY; PRT; 436 AA.

AC Q9ZKD7;

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1999, sequence version 1.

DT 21-FEB-2006, entry version 23.

DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.

GN Name=fucU; ORFNames=jhp_1002;

OS Helicobacter pylori J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Helicobacter.

OX NCBI_TaxID=85963;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;

RA Alm R.A., Ling L., S.-L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;

RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

RT Nature 397:176-180(1999).

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EMBL: AB001439; AAD06573.1; -; Genomic_DNA.

PIR: G71862; G71862.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008417; F:fucosyltransferase activity; IEA.

DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.

DR InterPro; IPR001503; Glyco_trans_10.

DR PANTHER; PTHR11929; Glyco_trans_10.

KW Complete proteome; Glycosyltransferase; Transferase.

SQ SEQUENCE 436 AA; 50699 MW; 1DBZ066AE98FA61E CRC64;

Query Match 86.3%; Score 2039; DB 2; Length 436;

Best Local Similarity 86.5%; Pred. No. 3.3e-130;

Matches 384; Conservative 25; Mismatches 23; Indels 12; Gaps 3;

QY 1 MFQPLLDAPFISASIKKMPLSY-----PPLKIAVANWVGAEFFKGGAMFILLSQRTITL 56

Db 1 MFQPLLDAPFISSTPIKK-KITFKSPPLKIAVANWVGAEFFKSTLYFILLSQRTITL 59

QY 57 HQNPNPSPDLVPGSPIGARKILSYQNTKRVFAGENEVFNFLDYAIGFDELDLRDRY 116

Db 60 HQNPNPSPDLVLGSPIGSARKILSYQNTKRVFTGENEVFNFLDYAIGFDELDLRDRY 119

QY 117 LRMPLYYDLRLHHKASVNDTTAPYKIKPDSLYTLKKPSHHFKKHPLCAVNVNDESDPLK 176

Db 120 LRMPLYYASLHYKASVNDTTAPYKIKNSLYALKKPSHHFKKHENHNLCAVNVNDESDPLK 179


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Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGDDEIKFKNVSLVFLSQRYYITLH 60
QY 58 QNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVNFNLFDYAIQFDELDLDRYL 117
Db 61 QNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVNFNLFDYAIQFDELDLDRYL 120
QY 118 RMPLYYDLRLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKHPLHCAVNDSDPLKR 177
Db 121 RMPLYYDLRLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKHPLHCAVNDSDPLKR 180
QY 178 GFASVASNPNAPKRNAPFYDALNSIEPTVGGGVKNTLYGKVGKNEFLSQYKFNLCFEN 237
Db 181 GFASVASNPNAPKRNAPFYDALNSIEPTVGGGVKNTLYGKVGKNEFLSQYKFNLCFEN 240
QY 238 SOGYGYVTEKIIDAIFSHSTPIYWGSPSVAKDNPKSFVNVHDFKNEDEAIDVYRLHTH 297
Db 241 TOGYGYVTEKIIDAIFSHSTPIYWGSPSVAKDNPKSFVNVHDFKNEDEAIDVYRLHTH 300
QY 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRLDNEPL 357
Db 301 KNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRLDNEPL 360
QY 358 VSIIDLRADYNLRLADYNLRLADYNLRLADYNLRLADYNLRLADYNLRLADYNLRLADYNL 396
Db 361 VTIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 420
QY 397 -----RLQNRSPLELSQNTTFKIYHKAHKSLLPLRAIRRWVKKLGL 440
Db 421 DLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLR 478

RESULT 4
QZSLI3_HELPJ
ID Q9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
AC Q9ZLI3_HELPJ
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA (1,3)-FUCOSYLTRANSFERASE.
GN Name=fucT; ORFNames=jhp_0596;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.B., Vovis G.P.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
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CC
CC EMBL; AE001439; AAD06169.1; -; Genomic_DNA.
DR PIR; B71914; B71914.
DR BiOCyc; HPYL85963:JHP0596-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR IncerPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glycosyltransferase; Transferase.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;

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Query Match 83.0%; Score 1960.5; DB 2; Length 454;
 Best Local Similarity 80.9%; Pred. No. 7.5e-125;

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Matches 368; Conservative 34; Mismatches 34; Indels 19; Gaps 3;
QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGDDEIKFKNVSLVFLSQRYYITL 56
Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGDDEIKFKNVSLVFLSQRYYITL 59
QY 57 HQNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVNFNLFDYAIQFDELDLDRY 116
Db 60 HQNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVNFNLFDYAIQFDELDLDRY 119
QY 117 RMPLYYDLRLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKHPLHCAVNDSDPLK 176
Db 120 RMPLYYDLRLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKHPLHCAVNDSDPLK 179
QY 177 RGFASVASNPNAPKRNAPFYDALNSIEPTVGGGVKNTLYGKVGKNEFLSQYKFNLCF 236
Db 180 RGFASVASNPNAPKRNAPFYDALNSIEPTVGGGVKNTLYGKVGKNEFLSQYKFNLCF 239
QY 237 NSQGYGYVTEKIIDAIFSHSTPIYWGSPSVAKDNPKSFVNVHDFKNEDEAIDVYRLHT 296
Db 240 NTQGYGYVTEKIIDAIFSHSTPIYWGSPSVAKDNPKSFVNVHDFKNEDEAIDVYRLHT 299
QY 297 HPNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRLDNEP 356
Db 300 HPNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRLDNEP 359
QY 357 LVSI -----DLRADYNLRLADYNLRLADYNLRLADYNLRLADYNLRLADYNLRLADYNL 402
Db 360 LVADIDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYD 419
QY 403 SPLELSQNTTFKIYHKAHKSLLPLRAIRRWVKK 437
Db 420 SPLELSQNTTFKIYHKAHKSLLPLRAIRRWVKK 454

RESULT 5
Q6ST35_HELPJ
ID Q6ST35_HELPJ PRELIMINARY; PRT; 432 AA.
AC Q6ST35_HELPJ
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Alpha-1,4 fucosyltransferase.
GN Name=fucTII;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=DSM 6709; DOI=10.1093/glycob/cw004;
RX PubMed=16000696; DOI=10.1093/glycob/cw004;
RA Rabbani S., Miksa V., Wipf B., Ernst B.;
RT "Molecular Cloning and Functional Expression of a Novel Helicobacter
RT pylori (alpha)-1,4 Fucosyltransferase.";
RL Glycobiology 15:1076-1083(2005).
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CC
CC EMBL; AY450598; AAR88243.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;

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Query Match 81.6%; Score 1927.5; DB 2; Length 432;
 Best Local Similarity 81.8%; Pred. No. 1.2e-122;
 Matches 360; Conservative 36; Mismatches 33; Indels 11; Gaps 3;

DR EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0008417; F:fucosyltransferase activity; IEA.
DR GO: 00016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO: 0006486; P:protein amino acid glycosylation; IEA.
DR InterPro: IPR001503; Glyco trans 10.
DR PANTHER; PTRI1929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;

Query Match 74.9%; Score 1769.5; DB 2; Length 462;
Best Local Similarity 72.3%; Pred. No. 7.4e-112;
Matches 336; Conservative 43; Mismatches 55; Indels 31; Gaps 57

Qy	1	MFQPLLDADFIESASIKQMPLSYPPKLIKAVANW----	GGAEFFKKSMYFILSORYITTL	56
Dd	1	MFQPLLDADFIDSTHLDLDE-TTHKPELVALANWVPLKNSEKKGFRD	FILHLFKQRYKIIL	59
Qy	57	HQNPNPESDLVFGSGPIGAARKILSYQNTKRVFYAGENEVPNFNLFDAIGA	DFDELDDRDY	116
Dd	60	HSPNPBPESDLVFGNPLEQARLKLSYQNTKRVFYTGENEVPNFNLFDAIGA	DFDELDFNDY	119
Qy	117	LRMPLYDYRLLHHKAESVNDTAPVKIKPDLSLYTLKPKSHHPKEKHPHLC	CAVVNDESPLK	176
Dd	120	LRMPLYAYILLHYXAMLVNDTTSPYYKLK--ALYTLLKPSHKPKENHNL	CALIHNESDPWK	177
Qy	177	RGFASFVASPNPAKRNAFYDALNSIEPVTVGGSGVKNTGLGVKVGKNEFL	SOYKFNLCPF	236
Dd	178	RGFASFVASPNPAIRNAFYDALNALIEPVASGGSVKNTGLGVKVGKNEFL	SOYKFNLCPF	237
Qy	237	NSQGYGVYTEKIIDAYSHTPTPIYWGSPSVAKOPNPKSFVNVDHFKNF	DEAIDVRYLHT	296
Dd	238	NSQGYGVYTEKILDAYSHTPTPIYWGSPSVAKOPNPKSFVNVDHFN	NFDEAIDVRYLHA	297
Qy	297	HPNAYDMLYENPLNTLDGKAYFYQDLSFPKKILDFFPKTILENDTIY	NNP----	353
Dd	298	HQNAYDMLYENPLNTLDGKAGFYQDLSFEKILDFPFKNILENDTIY	HCNDAHYSALHRDL	357
Qy	354	NEPLVSITDDLRLADYNVLRLADYNLRLADYNLRLADYN-----	----	396
Dd	358	NEPLVSVDLRRDHDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLR	VNYDDLRDHDHDLR	417
Qy	397	----RLIQNSPPLLELSQNTTFKIIYKHAYHKSFLPLRAIRRWVK	K 437	
Dd	418	RDHERULLSKATPLLLELSQNTSFKIYKAYOKSLPLRAIRRWVK	K 462	

RESULT 8
O32631 HELPY
ID AC O32631 HELPY PRELIMINARY; PRT; 333 AA.
AC O32631,
DT 01-JAN-1998, integrated into UniProtKB/TREMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-).
GN Name=fuct;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
RN NCBI_TaxID=210;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=NCTC 11637;
RX MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Bijnden D.H.,
RA Bird M.I.;
RT "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
RT alpha(1,3)-fucosyltransferase gene."
RL J. Biol. Chem. 272:21349-21356(1997).

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EMBL; AF006039; AAB93985.1; -, Genomic_DNA.
DR GO:0016020; C:membrane; IEA.
DR GO:0008417; F:fucosyltransferase activity; IEA.
DR GO:0016757; P:transferase activity, transferring glycosyl. . ; IEA.
DR GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro: IPR001503; GlycoTrans_10.
DR PANTHER: PTHR11929; GlycoTrans_10; 1.
DR Glyceroltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFPCBIAC127E0A8C CRC64;

Query Match 63.9%; Score 1509; DB 2; Length 333;
Best Local Similarity 84.1%; Pred. No. 2,5e-94;
Matches 280; Conservative 23; Mismatches 16; Indels 14; Gaps 1

QY 119 MPLYYDLRLHKAESVNDTTAPYKIPDLSLYTLTKPSHRFKPKPHLCAVVNDESPLKRG 178
DB 1 MPLYYDLRLHKAESVNDTTAPYKIKGNSLYTLTKPSHCFCFKNHPNLCALINNESDPLKRG 60

QY 179 PASFVASNPNAKRNAPFDALNSIEPTVTGGSGVKNTLGKYKGNKNEFLSOYKFNLCPENS 238
DB 61 PASFVASNANAPMENAIFYDALNSIEPTVTGGGAIVKNTLGKYKGNKSEFLSOYKFNLCPENS 120

QY 239 QGYGVVTEKIIDAYFSHTIPIYWGPSVAKPDPNPKSPVVNVHDFAIDVRYLHTHP 298
DB 121 QGYGVVTEKIIDAYFSHTIPIYWGPSVAKPDPNPKSPVVNVHDFAIDVRYLHTHP 180

QY 299 NAYLDMLYENPLNTLDGKAYFYQDSLFKKILDFKTILENDTIYHNPNPFVFYRDLNEPLV 358
DB 181 NAYLDMLYENPLNTLDGKAYFYQLSPFKILDFKTILENDTIYHNPNPFVFYRDLNEPLV 240

QY 359 SIDDLRADYNLRADYNLNLRADYNLNLRADYN-----RLQNRP 404
DB 241 SIDMLRINYDLNRVNYDDLVRVYDDLRLNYDDLRLNYDDLRLNYDDLRLNYDDLRLNQASP 300

QY 405 LLELSQNTTFKIYHKAYHKSPLRAIRRWYKK 437
DB 301 LLELSQNTSPFKIYRKIYQKSLPLRVRRWYKK 333

RESULT 9
QS1956 BACFN PRELIMINARY; PRT; 331 AA.
AC QS1956;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative LPS biosynthesis related glycosyltransferase.
GN OrderedLocustNames=BP3450;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Porton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Norton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
FT "Extensive DNA inversions in the B. fragilis genome control variable gene expression."
RL Science 307:1463-1465 (2005).

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EMBL; CR626927; CAH09151.1; -, Genomic_DNA.
DR GO:0016020; C:membrane; IEA.
DR GO:0008417; F:fucosyltransferase activity; IEA.
DR GO:0016740; P:transferase activity; IEA.
DR GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro: IPR002105; Dockerin 1.


```
QY 144 PDSLYTLKPSHFKEKPHLCVAVNDESDPLKRGFASVFNAPKRNAPFYDALNSTE 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 --NLX-LGDP-REFLERRDVNAIVAE-----KTRFCNLVCSNRAERLRFPEKLSRYK 144
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 PVTGGSVNTLGYKGNKNFSLQKFNLCFNSQGYVTEKLIIDAYFSTHPIYWG 263
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 PVDGSRVNNVGGVKDCLAPIRQHREPTIAFNASYPGYTEKIVPEMRVGSIPYWG 204
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 264 PSVAKDFNPKSFVNVDHDFKFNDEADIVYRYLTHPNAYLDMLYENPLNTLDCKAYFYQDL 323
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 PLVHLDFOLRSIVSWHSGSDEAALRVIQIDRDELYRHMLLOPPLP--EGRPTYSDF 262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 324 SPFKILDPFKTI 335
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 GV--LLDWLERV 272
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
Q54PJ9 D1CIDI PRELIMINARY; PRT; 462 AA.
AC Q54PJ9
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=DD0186041;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4; DOI=10.1038/nature03481;
RX PubMed=15875012; Gloeckner J.A., Gloeckner G., Rajandream M.A.,
RA Eichinger L., Pachebat J.A., Olsen R., Szafranski K., Xu Q.,
RA Sugang R., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Tunggal B., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Bankier A.T., Lehmann R., Saunders D., Sodergren E., Davis P.,
RA Pilcher K., Chen G., Hall N., Anjard C., Hemphill L., Bason N.,
RA Kerhornou A., Nie X., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBD whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; AAF101000108; EAL65179.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Golgi stack; Hypothetical protein; Transferase;
KW Transmembrane.
SQ SEQUENCE 462 AA; 54815 MW; 444843FFBAEF6D77 CRC64;
```

Query Match

8.9%; Score 210; DB 2; Length 462;

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Best Local Similarity 23.8%; Pred. No. 7.6e-06;
Matches 81; Conservative 64; Mismatches 127; Indels 68; Gaps 15;

QY 45 YFTLSQRYTITLQHPNPSDLVFGS-----PIGAARKILSVQNTKRVFYAGENEVFN-- 97
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 YIIVRKPY-----YFNQKLDMEINSDIYVDFEAPKKKLSRNVPRTLISMPO-PNRTC 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 184 EFDKCFEFPNFKVSFESQSDIRMGPDTPSSAYKLYNKLTIIDEIAKIQTQFKLE----Y 239
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QY 149 TLKPKSHHPEKHPHLCVAVNDESDPLKRGFASVFNAPKRNAPFYDALNSTEPTVGG 208
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 QVMK---HNNLTQPH-----QKSIPLANWFCNTCNHSHN---RNEYVQELMKFTIVVDSF 287
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 209 GS-----VKNLTGYKGVN-----KNEFLSQYKFNLCFNSQGYVTEKLIIDAYFSTIP 258
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 GKCLKMPNFTSNFLSRGSDPPFERKRLFITRYKFTIVFNSICKDYVSEKVLDAIAGSVP 347
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QY 259 IYWGSPSVAKDFNPKSFVNVDHDFKFNDEADIVYRYLTHPNAYLDMLYENPLNTLDGKAY 318
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Db 348 IFWGHPESTIKYPLNSYIFVGFQNAHLNHLKFLSENDEYF-----KLH 394
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QY 319 FYQDLSEFKKILDPFKTILENDTIYHNNPFVYRDLANEPLV 358
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Db 395 TWR--TNQTVIDQWKGV---NNYPNKGPRFRPREVQCPI 428
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RESULT 13
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AC Q54L56
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=DD0187176;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Quail M.A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
RA Sanders M., Ma J., Kohara Y., Hernandez J., Rabinowitsch E., Steffen D.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBD whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AAF101000141; EAL64002.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
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Query Match 8.2%; Score 193.5; DB 2; Length 417;
Best Local Similarity 24.8%; Pred. NO. 8.8e-05;
Matches 82; Conservative 49; Mismatches 89; Indels 111; Gaps 16;

DB 283 NIFDKRNFSNIE---DLILILNNMFDGEILKIL-E

283 NTPTDKRNP SNYE--DLYLYLKMPDGEYLYKYL-ENIENYLNSE----

Matches 82

Db :|:::
334 VQTVVQ 339

Search completed: August 11, 2006, 19:44:50
Job time : 158.087 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:45:14 ; Search time 30.1639 Seconds
(without alignments)
1276.805 Million cell updates/sec

Title: US-10-764-212-18

Perfect score: 2362

Sequence: 1 MFQPLLDFAIESASIKKMPK.....YHKSLLPLRAIRRWVKLGL 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2362	100.0	440	2	US-09-092-315-3
2	2362	100.0	440	2	US-09-733-524A-3
3	2362	100.0	440	2	US-10-189-977A-3
4	2362	100.0	440	3	US-10-392-098A-3
5	2015.5	85.3	454	2	US-09-092-315-8
6	2015.5	85.3	454	2	US-09-733-524A-8
7	2015.5	85.3	454	2	US-10-189-977A-8
8	2015.5	85.3	454	3	US-10-392-098A-8
9	1999	84.6	486	2	US-09-092-315-2
10	1999	84.6	486	2	US-09-733-524A-2
11	1999	84.6	486	2	US-10-189-977A-2
12	1999	84.6	486	3	US-10-392-098A-2
13	1983	84.0	464	2	US-09-092-315-1
14	1983	84.0	464	2	US-09-733-524A-1
15	1983	84.0	464	2	US-10-189-977A-1
16	1983	84.0	464	3	US-10-392-098A-1
17	1983	84.0	478	2	US-09-092-315-7
18	1982.5	83.9	476	2	US-09-092-315-5
19	1982.5	83.9	476	2	US-09-733-524A-5
20	1982.5	83.9	476	2	US-10-189-977A-5
21	1982.5	83.9	476	3	US-10-392-098A-5
22	1975	83.6	478	2	US-09-733-524A-7
23	1975	83.6	478	2	US-10-189-977A-7
24	1975	83.6	478	3	US-10-392-098A-7
25	1879.5	79.6	425	2	US-09-092-315-6
26	1879.5	79.6	425	2	US-09-733-524A-6

27	1879.5	79.6	425	2	US-10-189-977A-6	Sequence 6, Appli
28	1879.5	79.6	425	3	US-10-392-098A-6	Sequence 6, Appli
29	1742.5	73.8	372	2	US-09-092-315-13	Sequence 13, Appli
30	519	22.0	502	2	US-10-080-960-16	Sequence 16, Appli
31	154.5	6.5	139	2	US-10-080-960-18	Sequence 18, Appli
32	150	6.4	486	2	US-10-080-960-2	Sequence 2, Appli
33	137.5	5.8	433	2	US-09-092-315-11	Sequence 11, Appli
34	137.5	5.8	433	2	US-09-733-524A-11	Sequence 11, Appli
35	137.5	5.8	433	3	US-10-189-977A-11	Sequence 11, Appli
36	137.5	5.8	433	3	US-10-392-098A-11	Sequence 9, Appli
37	134.5	5.7	450	2	US-09-390-131-9	Sequence 3, Appli
38	134.5	5.7	451	2	US-09-390-131-3	Sequence 3100, Ap
39	126.5	5.4	915	2	US-09-583-110-3100	Sequence 8, Appli
40	124.5	5.3	405	1	US-07-914-281-8	Sequence 8, Appli
41	124.5	5.3	405	1	US-08-393-246-8	Sequence 8, Appli
42	124.5	5.3	405	1	US-08-525-058A-8	Sequence 8, Appli
43	124.5	5.3	405	1	US-08-696-731-8	Sequence 8, Appli
44	124.5	5.3	405	2	US-09-042-531-8	Sequence 8, Appli
45	123.5	5.2	357	5	PCT-US91-00899-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-092-315-3
; Sequence 3, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-3

Query Match	100.0%;	Score	2362;	DB 2;	Length	440;			
Best Local Similarity	100.0%;	Pred. No.	7.9e-224;						
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Db	1	MFQPLLDFAIESASIKKMPKLSYPPPLKIAVANWGGABEEFKKSAMYFILSORYTITLHQP	60						
Qy	61	NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNLFDYAIGFDELDRLDRYLMP	120						
Db	61	NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNLFDYAIGFDELDRLDRYLMP	120						
Qy	121	LYYDLRLHKAESVNDTPAPKIPDLSYTLTKPSHHFKKPHLCAVWVNDSDPLKRGFA	180						
Db	121	LYYDLRLHKAESVNDTPAPKIPDLSYTLTKPSHHFKKPHLCAVWVNDSDPLKRGFA	180						
Qy	181	SFVASPNAPKRNAPFDALNSIEPVTGGSGVKNTLYGKVGKNKEFLSQYKFNLCFENSQ	240						
Db	181	SFVASPNAPKRNAPFDALNSIEPVTGGSGVKNTLYGKVGKNKEFLSQYKFNLCFENSQ	240						
Qy	241	YGYVTEKIILDAVFSHTIPIYWGSPSVAKDFNPKSFVNVDHDKNFDEAIDVRYLHHPNA	300						
Db	241	YGYVTEKIILDAVFSHTIPIYWGSPSVAKDFNPKSFVNVDHDKNFDEAIDVRYLHHPNA	300						
Qy	301	YLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFFVYRDLNEPLVSI	360						
Db	301	YLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFFVYRDLNEPLVSI	360						


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RESULT 5
US-09-092-315-8
; Sequence 8, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8

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QY 1 MPQPLLDAPFIESAIKKN-PLSYPLKIAVANWGGAE--EFKISAMFYILSQRVTITLH 57

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Db      61 RNPDKPADIVFGNPLGSAKILSYQNTKRIFFYGENESPENPLFDVAIGFDELDRDYL 120
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Qy      178 GFASFVASNPAPKRNAPFDALNSIEPVTGGSVKNTLGYKVGKNKNEFLSQYKFNLCFEN 237
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Db      241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNPNFVYRDLNEPL 300
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Qy      404 PLELSONTTFKIIYKAYHKSLPLLRIRRWVKK 437
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RESULT 7
US-10-189-977A-8
; Sequence 8, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-8

Query Match      85.3%; Score 2015.5; DB 2; Length 454;
Best Local Similarity 83.0%; Pred. No. 1.1e-189;
Matches 377; Conservative 34; Mismatches 26; Indels 17; Gaps 3;

Qy      1 MFQPLLDAFIESASIKOM-PLSYPPLKIAVANWGGAB--EFKKSAMVFILSQHYTITLH 57
Db      1 MFQPLLDAFIESASIERMASKSPPLKIAVANWGGDEIEKEFKKSTLYFILSQHYTITLH 60
Qy      58 QNPNEPSDLVFGSPIGAAKILSYQNTKRVFYAGENEVPNPLFDVAIGFDELDRDYL 117
Db      61 RNPDKPADIVFGNPLGSAKILSYQNTKRIFFYGENESPENPLFDVAIGFDELDRDYL 120
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Db      121 RMPLYYDRLHHKAESVNDTTAPYKIKGNSLYTLKPSHCFCENHPNLCALINNESDPLKR 180

US-10-764-212-18.rai
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Db      241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNPNFVYRDLNEPL 300
Qy      298 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 357
Db      301 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 360
Qy      358 VSIDDLRADYNLADYNLADYNLADYNLADYNLADYNLADYNLADYNLADYNLADYNL 403
Db      361 VSIDNLRIYDNLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLR 420
Qy      404 PLELSONTTFKIIYKAYHKSLPLLRIRRWVKK 437
Db      421 PLELSONTSFKIYRKIYQKSLPLLRIRRWVKK 454

RESULT 8
US-10-392-098A-8
; Sequence 8, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1.3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11637
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-8

Query Match      85.3%; Score 2015.5; DB 3; Length 454;
Best Local Similarity 83.0%; Pred. No. 1.1e-189;
Matches 377; Conservative 34; Mismatches 26; Indels 17; Gaps 3;

Qy      1 MFQPLLDAFIESASIKOM-PLSYPPLKIAVANWGGAB--EFKKSAMVFILSQHYTITLH 57
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Qy      58 QNPNEPSDLVFGSPIGAAKILSYQNTKRVFYAGENEVPNPLFDVAIGFDELDRDYL 117
Db      61 RNPDKPADIVFGNPLGSAKILSYQNTKRIFFYGENESPENPLFDVAIGFDELDRDYL 120
Qy      118 RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKPSHHFKEKHPHLCAVNDSDPLKR 177
Db      121 RMPLYYDRLHHKAESVNDTTAPYKIKGNSLYTLKPSHCFCENHPNLCALINNESDPLKR 180
Qy      178 GFASFVASNPAPKRNAPFDALNSIEPVTGGSVKNTLGYKVGKNKNEFLSQYKFNLCFEN 237
Db      181 GFASFVASNANAPRNAPFDALNSIEPVTGGAVKNTLGYKVGKSEFLSQYKFNLCFEN 240
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[illegible]

RESULT 9

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US-09-092-315-2
; Sequence 2, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge. Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-2

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Query Match 84.6%; Score 1999; DB 2; Length 486;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28; Indels 4

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Qy	58	QNPNP	SDLVFG	SPIGAARK	ITLSQNTKRV	FAGENE	VPNPNL	PDYAL	GFDELDURDYL	117
Db	61	QNPNP	SDLVFG	SPIGARK	ITLSQNAKRV	FTYGENE	SPNPNL	PDYAL	GFDELDURDYL	120
Qy	118	RMPLY	YDRLHH	KAESVND	TTAPYKIKP	DSLTYL	KKPSHH	FKEGPHL	CAVNVNDESDPLKR	177
Db	121	RMPLY	YDRLHH	KAESVND	TTSPYKLP	DSLTYL	KKPSHH	FKENHPNL	CAVNVNDESDPLKR	180
Qy	178	GPASF	VASNP	AKGNAPYD	ALANSIEP	VTGGSG	VKNTLGYK	VGNKNE	FLSQYKNLCPEN	237
Db	181	GPASF	VASNP	AKGNAPYD	VLANSIEP	VTGGSG	VKNTLGYNI	KNKSE	FLSQYKNLCPEN	240
Qy	238	SOQGY	VTEKI	IDAYF	SHTIPIY	WGS	PSVAKDFNP	KSFVN	VHDPKNFDEADIVRYLH	297
Db	241	SOQGY	VTEKI	IDAYF	SHTIPIY	WGS	PSVAKDFNP	KSFVN	VHDPKNFDEADIVRYLH	300
Qy	298	PNAY	LDMLY	ENPLNTL	DGKAYFY	QDLSP	KKILD	FPFKTILE	NDTTYHNNPFFYFDRLNEPL	357
Db	301	PNAY	LDMLY	ENPLNTL	DGKAYFY	QNLSP	KKILD	FPFKTILE	NDTTYHNDPFFYFDRLNEPL	360
Qy	358	VSI-	-----	-----	-----	-----	-----	-----	-----	374
Db	361	IS	DDDLRVNY	DDLRVNY	DDLRVNY	DDLRVNY	DDLRVNY	DDLRVNY	DDLRVNY	420
Qy	375	NNLRADY	NNLRADY	NNLRADY	DRLLQNR	SPLELS	QNTFTFKI	YHKAYHKS	LPFLRAIRRW	434
Db	421	DDLRVNY	DDLRVNY	DDLRVNY	ERLONAS	PLELS	QNTFTFKI	YKAYOKS	PLPRAAACL	480

Qy 435 VKLGL 440
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Db 481 IKLGL 486

RESULT 10

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US-09-733-524A-2
; Sequence 2, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-733-524A-2

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Query Match 84.6%; Score 1999; DB 2; Length 486;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28; Indels 4

[illegible]

RESULT 11

US-10-189-977A-2
; Sequence 2, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-2

Query Match 84.6%; Score 1999; DB 2; Length 486;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;

QY 1 MFQPLDAFTESASIKKM-PLSYPPPLKIAVANWGG--AEEFKKSAMYFILSQRYTITLH 57
DB 1 MFQPLDAYIESASIEKITSKPPPLKIAVANWGGDEVEEFPKKNILYFILSQHYTITLH 60

QY 58 QNPNEPSDLVFGSPIGSARKILSYQNAKRVPYTGENSEPNFNLFDYAIGFDELDRYL 117
DB 61 QNPNEPSDLVFGSPIGSARKILSYQNAKRVPYTGENSEPNFNLFDYAIGFDELDRYL 120

QY 118 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKPHLCVAVNDESPLKR 177
DB 121 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKPHLCVAVNDESPLKR 180

QY 178 GFASFVSNPNAPKRNAPYDALNSTIEPVGGSVKNTLGYKVGKNEFLSQYKFNLCFEN 237
DB 181 GFASFVSNPNAPKRNAPYDALNSTIEPVGGSVKNTLGYKVGKNEFLSQYKFNLCFEN 240

QY 238 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDFDAIDYVRYLH 297
DB 241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDFDAIDYVRYLH 300

QY 298 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 357
DB 301 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 360

QY 358 VSI-----DRLADYNNLRADY 374
DB 361 ISIDDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNY 420

QY 375 NNLADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLR 434
DB 421 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 480

QY 435 VKKLGL 440
DB 481 IKKLGL 486

RESULT 12
US-10-392-098A-2
; Sequence 2, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1.3 Fucosyltransferase
FILE REFERENCE: 017398-0004200S
CURRENT APPLICATION NUMBER: US/10/392,098A
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 09/733,524
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 486
TYPE: PRT
ORGANISM: Helicobacter pylori
FEATURE:
OTHER INFORMATION: H. pylori strain UAL182
OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-2

Query Match 84.6%; Score 1999; DB 3; Length 486;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;

QY 1 MFQPLDAFTESASIKKM-PLSYPPPLKIAVANWGG--AEEFKKSAMYFILSQRYTITLH 57
DB 1 MFQPLDAYIESASIEKITSKPPPLKIAVANWGGDEVEEFPKKNILYFILSQHYTITLH 60

QY 58 QNPNEPSDLVFGSPIGSARKILSYQNAKRVPYTGENSEPNFNLFDYAIGFDELDRYL 117
DB 61 QNPNEPSDLVFGSPIGSARKILSYQNAKRVPYTGENSEPNFNLFDYAIGFDELDRYL 120

QY 118 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKPHLCVAVNDESPLKR 177
DB 121 RMPLYYDRLLHKAESVNDTTPYKIKPDSLYTLKKPSHHFKKPHLCVAVNDESPLKR 180

QY 178 GFASFVSNPNAPKRNAPYDALNSTIEPVGGSVKNTLGYKVGKNEFLSQYKFNLCFEN 237
DB 181 GFASFVSNPNAPKRNAPYDALNSTIEPVGGSVKNTLGYKVGKNEFLSQYKFNLCFEN 240

QY 238 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDFDAIDYVRYLH 297
DB 241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDFDAIDYVRYLH 300

QY 298 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 357
DB 301 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDFPKTILENDTIYHNNPFFVYRDLNEPL 360

QY 358 VSI-----DRLADYNNLRADY 374
DB 361 ISIDDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNY 420

QY 375 NNLADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLR 434
DB 421 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 480

QY 435 VKKLGL 440
DB 481 IKKLGL 486

RESULT 13
US-09-092-315-1
; Sequence 1, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming

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; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-1

Query Match      84.0%; Score 1983; DB 2; Length 464;
Best Local Similarity 80.8%; Pred. No. 1.8e-186;
Matches 375; Conservative 32; Mismatches 33; Indels 24; Gaps 3;

Qy 1 MFQPLDAFIESASIKKM-PLSYPLPKIAVANWGGAE--EFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLDAVVSASIEKMAKSPPLKIAVANWGGDEIKFKNVLYFILSQRYTITLH 60

Qy 58 QNPNEPSDLVFGSPIGAARKILSYQNTKRVYAGENEVFNPNFLDYAIGFDELDRDYL 117
Db 61 QNPNEFSDLVFCNPLGSAARKILSYQNAKRVFYTGENSEPNFLDYAIGFDELDFNDYL 120

Qy 118 RMPLYYDLRLHKAESVNDTTAPYKIPDSLYTLKKPSHHFKEKHPHLCVAVNDESDPLKR 177
Db 121 RMPLYYDLRLHKAESVNDTTAPYKIKNSLYALKPSHCFKHPHLCVAVNDESDPLKR 180

Qy 178 GFASFVSNPNAPKRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 237
Db 181 GFASFVSNPNAPIRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 240

Qy 238 SQGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH 297
Db 241 TOGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH 300

Qy 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYHNNPFFVYRDLEPL 357
Db 301 KNAYLDMLYENPLNTLDGKAYFYQNLSPKKILAFPKTLLENDTIYHDNPPFFICRDLNEPL 360

Qy 358 VSIDDLRADYNNLRADYNNLRADYNNLRADYD----- 396
Db 361 VTIDDLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVY 420

Qy 397 RLLQNRSPLELSQNTTPKIYKAYHKSPLRLAIRRWVKLGL 440
Db 421 RLLSKATPLELSQNTTSKIYKAYQKSLPLRLAIRRWVKLGL 464

RESULT 14
US-09-733-524A-1
; Sequence 1, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-733-524A-1

Query Match      84.0%; Score 1983; DB 2; Length 464;
Best Local Similarity 80.8%; Pred. No. 1.8e-186;
Matches 375; Conservative 32; Mismatches 33; Indels 24; Gaps 3;

Qy 1 MFQPLDAFIESASIKKM-PLSYPLPKIAVANWGGAE--EFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLDAVVSASIEKMAKSPPLKIAVANWGGDEIKFKNVLYFILSQRYTITLH 60

Qy 58 QNPNEPSDLVFGSPIGAARKILSYQNTKRVYAGENEVFNPNFLDYAIGFDELDRDYL 117
Db 61 QNPNEFSDLVFCNPLGSAARKILSYQNAKRVFYTGENSEPNFLDYAIGFDELDFNDYL 120

Qy 118 RMPLYYDLRLHKAESVNDTTAPYKIPDSLYTLKKPSHHFKEKHPHLCVAVNDESDPLKR 177
Db 121 RMPLYYDLRLHKAESVNDTTAPYKIKNSLYALKPSHCFKHPHLCVAVNDESDPLKR 180

Qy 178 GFASFVSNPNAPKRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 237
Db 181 GFASFVSNPNAPIRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 240

Qy 238 SQGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH 297
Db 241 TOGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH 300

Qy 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYHNNPFFVYRDLEPL 357
Db 301 KNAYLDMLYENPLNTLDGKAYFYQNLSPKKILAFPKTLLENDTIYHDNPPFFICRDLNEPL 360

Qy 358 VSIDDLRADYNNLRADYNNLRADYNNLRADYD----- 396
Db 361 VTIDDLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVY 420

Qy 397 RLLQNRSPLELSQNTTPKIYKAYHKSPLRLAIRRWVKLGL 440
Db 421 RLLSKATPLELSQNTTSKIYKAYQKSLPLRLAIRRWVKLGL 464
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; ORGANISM: Helicobacter pylori
US-09-733-524A-1

Query Match      84.0%; Score 1983; DB 2; Length 464;
Best Local Similarity 80.8%; Pred. No. 1.8e-186;
Matches 375; Conservative 32; Mismatches 33; Indels 24; Gaps 3;

Qy 1 MFQPLDAFIESASIKKM-PLSYPLPKIAVANWGGAE--EFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLDAVVSASIEKMAKSPPLKIAVANWGGDEIKFKNVLYFILSQRYTITLH 60

Qy 58 QNPNEPSDLVFGSPIGAARKILSYQNTKRVYAGENEVFNPNFLDYAIGFDELDRDYL 117
Db 61 QNPNEFSDLVFCNPLGSAARKILSYQNAKRVFYTGENSEPNFLDYAIGFDELDFNDYL 120

Qy 118 RMPLYYDLRLHKAESVNDTTAPYKIPDSLYTLKKPSHHFKEKHPHLCVAVNDESDPLKR 177
Db 121 RMPLYYDLRLHKAESVNDTTAPYKIKNSLYALKPSHCFKHPHLCVAVNDESDPLKR 180

Qy 178 GFASFVSNPNAPKRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 237
Db 181 GFASFVSNPNAPIRNAPFYDALNSIEPTVGGSGVKNLTGYKVGKNKNEFLSQYKFNLCFEN 240

Qy 238 SQGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH 297
Db 241 TOGYGVVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH 300

Qy 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYHNNPFFVYRDLEPL 357
Db 301 KNAYLDMLYENPLNTLDGKAYFYQNLSPKKILAFPKTLLENDTIYHDNPPFFICRDLNEPL 360

Qy 358 VSIDDLRADYNNLRADYNNLRADYNNLRADYD----- 396
Db 361 VTIDDLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVYDRLRVY 420

Qy 397 RLLQNRSPLELSQNTTPKIYKAYHKSPLRLAIRRWVKLGL 440
Db 421 RLLSKATPLELSQNTTSKIYKAYQKSLPLRLAIRRWVKLGL 464

RESULT 15
US-10-189-977A-1
; Sequence 1, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-1

Query Match      84.0%; Score 1983; DB 2; Length 464;
Best Local Similarity 80.8%; Pred. No. 1.8e-186;
Matches 375; Conservative 32; Mismatches 33; Indels 24; Gaps 3;

Qy 1 MFQPLDAFIESASIKKM-PLSYPLPKIAVANWGGAE--EFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLDAVVSASIEKMAKSPPLKIAVANWGGDEIKFKNVLYFILSQRYTITLH 60
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Db      1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKEFKNSVLIFYILSQRYTITLH 60
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Db      61 QNPNESDLVFGNPLGSARKILSYQNAKRIFYTGENESPNNLFDYAIGFDELDLDRYL 120
Qy     118 RMPLYYDRLHKKAESVNDTTAPYKIKPDSLYTLKCPSHHFKKHPHLCVVNDESDPLKR 177
Db     121 RMPLYYDRLHKKAESVNDTTAPYKLDNSLYALKPSHCFKHPNLCAVVNDESDPLKR 180
Qy     178 GFASFVASNPNAPKRNAFYDALNSIEPVTCGGSVKNTLYGKVGKNKNEFLSQYKFNLCFEN 237
Db     181 GFASFVASNPNAPIRNAFYDALNSIEPVTCGGSVRNTLGYNVKNKNEFLSQYKFNLCFEN 240
Qy     238 SQGYGYVTEKIIDAYFSHTTIPYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLH 297
Db     241 TQGYGYVTEKIIDAYFSHTTIPYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLH 300
Qy     298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYHNNPFVYRDLNEPL 357
Db     301 KNAYLDMLYENPLNTLDGKAYFYQNLSPKKILAFFKTIENDTIYHNDPIFCRDLNEPL 360
Qy     358 VSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNN 396
Db     361 VTIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYE 420
Qy     397 RLQNRSPLELSEONTTFKLYHKAYHKSPLRLRAIRRWVKKLGL 440
Db     421 RLLSKATPPLLELSEONTTSKIYRKAYQKSLPLRLRAIRRWVKKLGL 464
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Search completed: August 11, 2006, 19:47:32
Job time : 32.1639 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:46:14 ; Search time 107.213 Seconds
(without alignments)
1901.022 Million cell updates/sec

Title: US-10-764-212-18

Perfect score: 2362

Sequence: 1 MFQPLDAFIESASIKKMPK.....YHKSLPLRAIRWWVKLGL 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2362	100.0	440	4	US-10-120-319-3
2	2362	100.0	440	4	US-10-189-977-3
3	2362	100.0	440	4	US-10-392-098-3
4	2362	100.0	440	5	US-10-764-212-18
5	2347	99.4	440	3	US-09-733-524-3
6	2015.5	85.3	454	4	US-10-120-319-8
7	2015.5	85.3	454	4	US-10-189-977-8
8	2015.5	85.3	454	4	US-10-392-098-8
9	2007.5	85.0	485	5	US-10-764-212-6
10	2006.5	84.9	454	3	US-09-733-524-18
11	1999	84.6	486	4	US-10-120-319-2
12	1999	84.6	486	4	US-10-189-977-2
13	1999	84.6	486	4	US-10-392-098-2
14	1999	84.6	486	5	US-10-764-212-2
15	1984.5	84.0	485	3	US-09-733-524-2
16	1983	84.0	464	4	US-10-120-319-1
17	1983	84.0	464	4	US-10-189-977-1
18	1983	84.0	464	4	US-10-392-098-1
19	1983	84.0	478	4	US-10-120-319-7
20	1983	84.0	478	4	US-10-189-977-7
21	1982.5	83.9	476	3	US-09-733-524-15
22	1982.5	83.9	476	4	US-10-120-319-5
23	1982.5	83.9	476	4	US-10-189-977-5
24	1982.5	83.9	476	4	US-10-392-098-5
25	1975	83.6	478	4	US-10-392-098-7
26	1970.5	83.4	432	5	US-10-764-212-4
27	1970	83.4	501	3	US-09-733-524-1

28	1963	83.1	436	4	US-10-335-977-8559	Sequence 8559, Ap
29	1960.5	83.0	479	3	US-09-733-524-17	Sequence 17, Appl
30	1924.5	81.5	421	4	US-10-335-977-8558	Sequence 8558, Ap
31	1879.5	79.6	425	4	US-10-120-319-6	Sequence 6, Appli
32	1879.5	79.6	425	4	US-10-189-977-6	Sequence 6, Appli
33	1879.5	79.6	425	4	US-10-392-098-6	Sequence 12, Appl
34	1879.5	79.6	425	5	US-10-764-212-12	Sequence 16, Appl
35	1869	79.1	424	3	US-09-733-524-16	Sequence 16, Appl
36	1861	78.8	446	5	US-10-764-212-16	Sequence 68, Appl
37	1793	75.9	377	5	US-10-764-212-68	Sequence 66, Appl
38	1786.5	75.6	391	5	US-10-764-212-66	Sequence 13, Appl
39	1742.5	73.8	372	4	US-10-120-319-13	Sequence 13, Appl
40	1742.5	73.8	372	4	US-10-189-977-13	Sequence 20, Appl
41	1737.5	73.6	456	5	US-10-764-212-20	Sequence 8, Appli
42	1187.5	50.3	277	5	US-10-764-212-8	Sequence 70, Appl
43	1146	48.5	256	5	US-10-764-212-70	Sequence 75, Appl
44	1145.5	48.5	246	5	US-10-764-212-75	Sequence 74, Appl
45	1141.5	48.3	246	5	US-10-764-212-74	

ALIGNMENTS

RESULT 1
US-10-120-319-3
; Sequence 3, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-3

Query Match	100.0%	Score 2362;	DB 4;	Length 440;
Best Local Similarity	100.0%	Pred. No. 4.1e-192;		
Matches 440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFQPLDAFIESASIKKMPLSYPPPLKIAVANWGGAEFFKKSAMYFILSORYTITLHQP	60	
Db	1	MFQPLDAFIESASIKKMPLSYPPPLKIAVANWGGAEFFKKSAMYFILSORYTITLHQP	60	
QY	61	NEPSDLVFGSPGAAARKILSYONTKRVFVYAGENEVENFNLDVAIGFDELDLDRYLRLMP	120	
Db	61	NEPSDLVFGSPGAAARKILSYONTKRVFVYAGENEVENFNLDVAIGFDELDLDRYLRLMP	120	
QY	121	LYYDLRHKHAESVNDTTAPYKIKPDSLYTLKKPSHFHFKKHPLCAVNVNDESPLKRGFA	180	
Db	121	LYYDLRHKHAESVNDTTAPYKIKPDSLYTLKKPSHFHFKKHPLCAVNVNDESPLKRGFA	180	
QY	181	SFVASNPAPKRNAPFYDALNSIEPVTGGGSKVNTLGKYGKGNKVEFTISQYKFNLCFENSQ	240	
Db	181	SFVASNPAPKRNAPFYDALNSIEPVTGGGSKVNTLGKYGKGNKVEFTISQYKFNLCFENSQ	240	
QY	241	YGYVTEKILIDAYFSHTIPIYWGSPSVAKDPNPKSFVNVDHFKNFDAIDVRYLHTHPNA	300	
Db	241	YGYVTEKILIDAYFSHTIPIYWGSPSVAKDPNPKSFVNVDHFKNFDAIDVRYLHTHPNA	300	
QY	301	YLDMLYENPLNTLDGKAFYQDLSFKKILDDFFKTLILENDTIYHNNPFVYRDLNEPLVSI	360	
Db	301	YLDMLYENPLNTLDGKAFYQDLSFKKILDDFFKTLILENDTIYHNNPFVYRDLNEPLVSI	360	


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; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/1.0/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 802 Futa fucosyltransferase
US-10-764-212-18

Query Match      100.0%; Score 2362; DB 5; Length 440;
Best Local Similarity 100.0%; Pred. No. 4.1e-192;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1 MFQPLLDADFATESASIKKMPILSYPPPLKIADVANNWGGAESEFKKSAMFYLLSQRYTITLHQP 60
DB    1 MFQPLLDADFATESASIKKMPILSYPPPLKIADVANNWGGAESEFKKSAMFYLLSQRYTITLHQP 60

QY    61 NEPSDLVFGSPIGAARKILSYONTKRVPFYAGENEVFNFLFDYAIGFDELDLRDYLRLMP 120
DB    61 NEPSDLVFGSPIGAARKILSYONTKRVPFYAGENEVFNFLFDYAIGFDELDLRDYLRLMP 120

QY    121 LYDRLRHHKAESVNDTTAPYKIKPDSLYTLKKPSHPHKPKPHLCVAVNDESDDLKRGFA 180
DB    121 LYDRLRHHKAESVNDTTAPYKIKPDSLYTLKKPSHPHKPKPHLCVAVNDESDDLKRGFA 180

QY    181 SFVASPNAPKRNAPYDALNISIEPVGTGGSVNQLGYKVGNKNFEFLSQYKFNLCFENSQG 240
DB    181 SFVASPNAPKRNAPYDALNISIEPVGTGGSVNQLGYKVGNKNFEFLSQYKFNLCFENSQG 240

QY    241 YGVYTEKIIDAYFSHTPIYWGSSPSVAKDFNPKSFVNVDPKNRPDEADIVYRLTHPNA 300
DB    241 YGVYTEKIIDAYFSHTPIYWGSSPSVAKDFNPKSFVNVDPKNRPDEADIVYRLTHPNA 300

QY    301 YLDMLEYENPLNLTDGKAFYQDLISFKKILDFFKITLENDTIYHNPNPFYFRDLNEPLVSI 360
DB    301 YLDMLEYENPLNLTDGKAFYQDLISFKKILDFFKITLENDTIYHNPNPFYFRDLNEPLVSI 360

QY    361 DDLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRL 420
DB    361 DDLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRLRADYNRL 420

QY    421 YHKSPLPLRAIRRWVKLGL 440
DB    421 YHKSPLPLRAIRRWVKLGL 440

RESULT 5
US-09-733-524-3
; Sequence 3, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPOSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 440
; TYPE: PRT
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[illegible]


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; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-2

Query Match      84.6%; Score 1999; DB 4; Length 486;
Best Local Similarity 77.6%; Pred. No. 3.6e-161;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;

Qy 1 MFQPLLDAFIESASIKKM-PLSYPPKIAVANWGG--AEEFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLLDAYIESASIEKITSKPPPLKIAVANWGDVEEVEEFKKNILYFILSQHYTITLH 60
Qy 58 QNPNEPSDLVFGSPIGSARKILSYQNAKRVFTYGENESPENFNLFDYAIGFDELDFRDYL 117
Db 61 QNPNEPSDLVFGSPIGSARKILSYQNAKRVFTYGENESPENFNLFDYAIGFDELDFRDYL 120
Qy 118 RMPLYYDRLLHKAESVNDTTAPYKIKPDSLTYLTKPSSHFKKHPHLCVAVNDESPLKR 177
Db 121 RMPLYYDRLLHKAESVNDTTSPYKLPDLSYALKPKSSHFKKHPHLCVAVNDESPLKR 180
Qy 178 GFASFVSNPNAPKRNAPFVDALNSTEPTVGGGSKVNTLGYKVGKNKEFSLQYKFNLCFEN 237
Db 181 GFASFVSNPNAPKRNAPFVDVLSNTEPTVGGGSKVNTLGYNIKNKSEFSLQYKFNLCFEN 240
Qy 238 SQGYGYVTEKIIDAYFSHTIPIYWGSPSAQDFNPKSFVNVDHFKNFDBAIDYVRYLHTH 297
Db 241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSAQDFNPKSFVNVDHFKNFDBAIDYVRYLHTH 300
Qy 298 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRDLNEPL 357
Db 301 PNAVLDMLYENPLNTLDGKAYFYQNLSPKKILDPFKTILENDTIYHNDNPFIFYRDLNEPL 360
Qy 358 VSI-----DDLRADYNNLRADY 374
Db 361 ISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 420
Qy 375 NNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADY 434
Db 421 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 480
Qy 435 VKKGL 440
Db 481 IKKGL 486

RESULT 13
US-10-392-098-2
; Sequence 2, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-2

Query Match      84.6%; Score 1999; DB 4; Length 486;
Best Local Similarity 77.6%; Pred. No. 3.6e-161;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;

Qy 1 MFQPLLDAFIESASIKKM-PLSYPPKIAVANWGG--AEEFKKSAMFYILSQRYTITLH 57
Db 1 MFQPLLDAYIESASIEKITSKPPPLKIAVANWGDVEEVEEFKKNILYFILSQHYTITLH 60
Qy 58 QNPNEPSDLVFGSPIGSARKILSYQNAKRVFTYGENESPENFNLFDYAIGFDELDFRDYL 117
Db 61 QNPNEPSDLVFGSPIGSARKILSYQNAKRVFTYGENESPENFNLFDYAIGFDELDFRDYL 120
Qy 118 RMPLYYDRLLHKAESVNDTTAPYKIKPDSLTYLTKPSSHFKKHPHLCVAVNDESPLKR 177
Db 121 RMPLYYDRLLHKAESVNDTTSPYKLPDLSYALKPKSSHFKKHPHLCVAVNDESPLKR 180
Qy 178 GFASFVSNPNAPKRNAPFVDALNSTEPTVGGGSKVNTLGYKVGKNKEFSLQYKFNLCFEN 237
Db 181 GFASFVSNPNAPKRNAPFVDVLSNTEPTVGGGSKVNTLGYNIKNKSEFSLQYKFNLCFEN 240
Qy 238 SQGYGYVTEKIIDAYFSHTIPIYWGSPSAQDFNPKSFVNVDHFKNFDBAIDYVRYLHTH 297
Db 241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSAQDFNPKSFVNVDHFKNFDBAIDYVRYLHTH 300
Qy 298 PNAVLDMLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVYFRDLNEPL 357
Db 301 PNAVLDMLYENPLNTLDGKAYFYQNLSPKKILDPFKTILENDTIYHNDNPFIFYRDLNEPL 360
Qy 358 VSI-----DDLRADYNNLRADY 374
Db 361 ISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY 420
Qy 375 NNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADY 434
Db 421 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 480
Qy 435 VKKGL 440
Db 481 IKKGL 486

RESULT 12
US-10-189-977-2
; Sequence 2, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
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; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-2

Query Match      84.6%; Score 1999; DB 4; Length 486;
Best Local Similarity 77.6%; Pred. No. 3.6e-161;
Matches 377; Conservative 35; Mismatches 28; Indels 46; Gaps 3;

QY 1 MFQPLLDAPIESASTKKM-PLSYPPPLKIAVANWGG--AEEPKKSAMYPILSORYTITLH 57
DB 1 MFQPLLDAYIESASTEKITSKPPPLKIAVANWGGDEEVEEFKKNLILYFILSQHYTITLH 60
QY 58 QNPNEPSDLVFGSPIGSARKILSYQNTKRVFYAGENEVNFNLFDAIGAIGFDELDRDYL 117
DB 61 QNPNEPSDLVFGSPIGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGAIGFDELDRDYL 120
QY 118 RNPYYDRLHHKAEVNDTTAPYKIPDSLYTLKKPSHHFKKPHLCAVNNDESPLKR 177
DB 121 RNPYYDRLHHKAEVNDTTSPYKLPDSLYALKKPSHHFKKPHLCAVNNDESPLKR 180
QY 178 GFASFVASNPNAPKRNAPFYDALNSTEPVTGGSVKNTLGYKVGKNEFLSQYKFNLCFEN 237
DB 181 GFASFVASNPNAPKRNAPFYDVNLSTEPVIGGSGVKNLTGYNIKNSKSEFLSQYKFNLCFEN 240
QY 238 SQGYGVVTEKIIDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHDFKMFDEAIDVRYLH 297
DB 241 SQGYGVVTEKIIDAYFSHTPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLH 300
QY 298 PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTLTLENDTIYHNNPFFVYRDLNEPL 357
DB 301 PNAYLDMLYENPLNTLDGKAYFYQNLSPKILDFKTLTLENDTIYHNDPFIYRDLNEPL 360
QY 358 VSI-----DOLRADYNNLRADY 374
DB 361 ISIDDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVY 420
QY 375 NNLRADYNNLRADYNNLRADYDLRLQNSPILLESQNTTFKIYHKAYHKSPLLRAIRRW 434
DB 421 DDLRVYDDLVRVYDDLVRVYERLLQNASPILLESQNTTFKIYKAYOKSLPLLRAR 480
QY 435 VKLGL 440
DB 481 IKLGL 486

RESULT 15
US-09-733-524-2
; Sequence 2, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 1182 from UAI182
US-09-733-524-2

Query Match      84.0%; Score 1984.5; DB 3; Length 485;
Best Local Similarity 77.6%; Pred. No. 6.1e-160;
Matches 377; Conservative 34; Mismatches 28; Indels 47; Gaps 4;

; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-764-212-2

Query Match      84.6%; Score 1999; DB 5; Length 486;
Best Local Similarity 77.6%; Pred. No. 3.6e-161;
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:47:49 ; Search time 16.7213 Seconds
(without alignments)
1771.230 Million cell updates/sec

Title: US-10-764-212-18

Perfect score: 2362

Sequence: 1 MFQPLLDATFASIKRMPL.....YHKSILPLRAIRRWVKLGL 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	6.7	302	6	US-10-953-349-5129
2	159	6.7	323	6	US-10-953-349-5128
3	159	6.7	338	6	US-10-953-349-5127
4	145.5	6.2	246	6	US-10-449-902-44967
5	141	6.0	406	7	US-11-197-712-284
6	132	5.6	513	6	US-10-449-902-52598
7	116.5	4.9	954	6	US-10-537-642-8
8	115	4.9	1791	6	US-10-537-642-18
9	113.5	4.8	336	7	US-11-293-697-4748
10	112.5	4.8	1062	6	US-10-537-642-6
11	111.5	4.7	2538	7	US-11-375-551-20
12	111.5	4.7	2538	7	US-11-070-573-23
13	111.5	4.7	4995	7	US-11-070-573-60
14	111.5	4.7	5001	7	US-11-070-573-68
15	110	4.7	3029	6	US-10-537-642-10
16	109.5	4.6	871	6	US-10-527-411-2
17	109.5	4.6	871	6	US-10-527-411-8
18	109.5	4.6	871	6	US-10-527-411-26
19	109.5	4.6	871	6	US-10-527-411-153
20	109.5	4.6	871	6	US-10-527-411-155
21	109.5	4.6	873	6	US-10-527-411-149
22	109.5	4.6	873	6	US-10-527-411-151
23	109.5	4.6	873	6	US-10-527-411-163
24	109.5	4.6	873	6	US-10-527-411-165
25	109.5	4.6	873	6	US-10-527-411-167

26	109.5	4.6	873	6	US-10-527-411-169
27	109.5	4.6	879	6	US-10-527-411-159
28	109.5	4.6	1127	6	US-10-527-411-40
29	109.5	4.6	1129	6	US-10-527-411-42
30	108	4.6	454	6	US-10-527-411-74
31	108	4.6	1130	6	US-10-527-411-139
32	107.5	4.6	737	6	US-10-505-928-608
33	107.5	4.6	737	7	US-11-300-928-30
34	107.5	4.6	742	6	US-10-471-571A-1894
35	107	4.5	866	6	US-10-527-411-32
36	107	4.5	875	6	US-10-527-411-10
37	107	4.5	876	6	US-10-527-411-66
38	107	4.5	878	6	US-10-527-411-62
39	107	4.5	879	6	US-10-527-411-30
40	107	4.5	908	6	US-10-527-411-64
41	107	4.5	914	6	US-10-527-411-60
42	107	4.5	949	6	US-10-527-411-68
43	107	4.5	1130	6	US-10-527-411-44
44	107	4.5	1132	6	US-10-527-411-46
45	105.5	4.5	457	6	US-10-527-411-70

ALIGNMENTS

RESULT 1
US-10-953-349-5129
; Sequence 5129, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5129
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5129

Query Match 6.7%; Score 159, DB 6; Length 302;
Best Local Similarity 25.1%; Pred. No. 1.5e-05;
Matches 70; Conservative 45; Mismatches 94; Indels 70; Gaps 12;

QY	176	KEGFASFVASNPNAKRNAFYDAL-----NSTEPVTGGGSKVNTLGYKVGKNKNEFLSQYK	230
Db	9	ERAIAAAFISNGA--RNFRLOALEAMKMTNLIKIDSYGGCHNRDG-KV-DKVEALKRYK	64
QY	231	FNLCPENSQGYGVTEKIIDAYFSHTPIYWGSPSVAKDFNP--KSFVNVHDFKNFDEAI	288
Db	65	FSLAFTENNEEDYVTEKPFQSLVAGSVVPVVGPPNI-BEPAPASDSFLHIKTMEDVEPVA	123
QY	289	DYRVYLTHPNAYLDM-----YENPLNTLDGKAYFYODLSFKKILD-----FFK	333
Db	124	KMKYLAANPAAYNOTLRWKYEGPSD-----SFKALVDMAAVHSSCRCLCIFLA	171
QY	334	TITLE-----NDTIYHNPFFVFRDLNEPLVSDIDDLADYNNLRAD	373
Db	172	TKVRQEEESPNFKRCKCSRGSGSDTVYH-----VFVRGRGFEMESVFLRGKSVTOEAL	227
QY	374	YNNLRADYNNLRADY-----NNLRADYDRLIQNRSP	405
Db	228	ESAVLAKPKSLKHEAVWKERPGLNKGDKELKHRIYPL	266

RESULT 2
US-10-953-349-5128
; Sequence 5128, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5128
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5128

Query Match 6.7%; Score 159; DB 6; Length 323;
Best Local Similarity 25.1%; Pred. No. 1.8e-05;
Matches 70; Conservative 45; Mismatches 94; Indels 70; Gaps 12;

Qy 176 KRGFASVSNPNAPKNAFYDAL-----NSIEPTVGGGVKNTLGYKVGKNEFLSQYK 230
Db 30 ERAIAAFISNCGA--RNFRLOALEALMKTNIKIDSYGGCHNRDG-KV-DKVEALKRYK 85

Qy 231 FNLCFENSQGVYVTEKIIDAYFSHTIPIYWGSPSVAKDFNP--KSFVNVHDFKFNDEAI 288
Db 86 FSLAFENTNEEDYVTEKFQSLVAGSVFVVGPPNI-BEAPASDSFLHIKTMEDVEPVA 144

Qy 289 DYVRYLTHPNAYLDML---YENPLNTLDGKAYFYQDLSFKKILD-----FFK 333
Db 145 KRMKYLAANPAAYNQTLRWKYEGPSD-----SPKALVDMAAVHSSCRLCIFLA 192

Qy 334 TILF-----NDTIYNNPFFVYRDLEPLVSIDDLRADYNNLRAD 373
Db 193 TRVREQEESPNFKRCKSRGSGSDTVYH-----VFRERGRFEMESVFLRGKSVTQEAL 248

Qy 374 YNNLRADYNNLRADY-----NNLRADYDRLLQNRSL 405
Db 249 ESAVLAKFKSLKHEAVKWKERPGNLKGDKEKELHIHRIYPL 287

RESULT 3
US-10-953-349-5127
; Sequence 5127, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5127
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5127

Query Match 6.7%; Score 159; DB 6; Length 338;
Best Local Similarity 25.1%; Pred. No. 1.8e-05;
Matches 70; Conservative 45; Mismatches 94; Indels 70; Gaps 12;

Qy 176 KRGFASVSNPNAPKNAFYDAL-----NSIEPTVGGGVKNTLGYKVGKNEFLSQYK 230
Db 45 ERAIAAFISNCGA--RNFRLOALEALMKTNIKIDSYGGCHNRDG-KV-DKVEALKRYK 100

Qy 231 FNLCFENSQGVYVTEKIIDAYFSHTIPIYWGSPSVAKDFNP--KSFVNVHDFKFNDEAI 288
Db 101 FSLAFENTNEEDYVTEKFQSLVAGSVFVVGPPNI-BEAPASDSFLHIKTMEDVEPVA 159

Qy 289 DYVRYLTHPNAYLDML---YENPLNTLDGKAYFYQDLSFKKILD-----FFK 333
Db 287

Db 160 KRMKYLAANPAAYNQTLRWKYEGPSD-----SPKALVDMAAVHSSCRLCIFLA 207
Qy 334 TILF-----NDTIYNNPFFVYRDLEPLVSIDDLRADYNNLRAD 373
Db 208 TRVREQEESPNFKRCKSRGSGSDTVYH-----VFRERGRFEMESVFLRGKSVTQEAL 263
Qy 374 YNNLRADYNNLRADY-----NNLRADYDRLLQNRSL 405
Db 264 ESAVLAKFKSLKHEAVKWKERPGNLKGDKEKELHIHRIYPL 302

RESULT 4
US-10-449-902-44967
; Sequence 44967, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205YI-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44967
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44967

Query Match 6.2%; Score 145.5; DB 6; Length 246;
Best Local Similarity 24.5%; Pred. No. 0.00015;
Matches 52; Conservative 31; Mismatches 92; Indels 37; Gaps 6;

Qy 117 LRMPLYD-RLHHAESVNDTTPYKIKPDSLYTLKPSHHFKHPHCAVND-----170
Db 4 LPLRYLDLEAARKPTGFEDIFGVHAKDDVQVTVAGKSFTSRSHVSTEKENDALIYV 63

Qy 171 -----ESDPLKRGFASVSNPNAPKNAFYDALNSIEPTVGGSVKNTLGYKVGK 223
Db 64 SSSRCLPHRDVAKDFLSLV-----PHHSFGKCLNNVD---GPDMAISM-YPCVSTN 111

Qy 224 E-----FLSQYKFNLCFENSQGVYVTEKIIDAYFSHTIPIYWGSPSVAKDFN 271
Db 112 DNGKPHWHDHLHCAMSHYKFKVLAIENTKTESVTEKLFYALEAGSVPIIFGAPNVWDFIP 171

Qy 272 PKSFVNVHDFKNFDRDAIDYVRYLTHPNAYLD 303
Db 172 PMSIIDASKFSLSRELASVYKAVANDPVAYAE 203

RESULT 5
US-11-197-712-284
; Sequence 284, Application US/11197712
; Publication No. US20060130160A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US4.CIP
; CURRENT APPLICATION NUMBER: US/11/197,712
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/876,997
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07


```
Db 412 -PFHK 415
:|
US-10-537-642-18
; Sequence 18, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1791
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-18

Query Match 4.9%; Score 115; DB 6; Length 1791;
Best Local Similarity 18.6%; Pred. No. 0.9;
Matches 93; Conservative 80; Mismatches 156; Indels 170; Gaps 25;

Qy 37 BEPKSAMVFTLSORYTITLHONNEPSDLVFGSPIGAARKILSY--ONTKRVF-YAGEN 93
Db 931 EDISK-----MOKYFLHSHKHK-----QIEDKXTHYFKHNVSCVTPYAGNN 976
Qy 94 EVPNFNLD---YAIG-FDELDRDRYLRMPLYDRLHKAESVNDTT--APYKIKPDSL 147
Db 977 INHNFNRKRYKSYNLYDHLDEQIKGKKYFNKDKELIGSINKQTERPKKKKNGNI 1036
Qy 148 YTLKP-----SHFKEKPHLCVND-----SDPLKRGFASVSNPNAPKR----- 192
Db 1037 ENKDKKKIRMITNKTKEKHSNIIISVEQNMHFNNSLKKCVNFTGKNEBYLARANTNC 1096
Qy 193 -----NAFY-----DALNSIEPVTVGGG-----VKNTLGVKV 219
Db 1097 SLGKEMEEDVYFHSNNIYNNQTSYDIDNTTKLGMGNNTNDISKNGKNGKJGKI 1156
Qy 220 G-----KNNEFLSQYKFNLCFENSQGYGVVTEKIIDA----YFSHTIPIYMGSPVA 267
Db 1157 SFFSMNNKYHSEIMNEE-----DNKNMNLTSQIINKDKYNYFTH-----CPSLK 1203
Qy 268 KDFNPKSFVNVHD-FKXNPFDEAIDYVRYLHTHPNAYLMDLYENPLNTLDGKAYFYQDLSFK 326
Db 1204 K--KKSVFTKINNLFKNYFKSID-----VHKEKFGFS 1232
Qy 327 KILDPFKTILENDT-----YHNNPFVFRDLNEPLVSIIDDLRADYNLADY- 374
Db 1233 KKFVFSK--DSDDIKGNNNKISKNNRYNN-----NNNNNSYNSIDSKYSHNNKNNHH 1286
Qy 375 -NNLRADYNLNRADYN-----LRADYDRLQNRSPLELSQNTTFFKIYHK 419
Db 1287 NNNKYHHNNKYHHNNKYHHNNKYHHNNKYHHNNKYHHNNKYHHNNKYHHNNKYHHNN 1346
Qy 420 AYHKSLLPLLRAIRWVKL 438
Db 1347 NYDKKL-----LKKL 1356

RESULT 9
US-11-293-697-4748
; Sequence 4748, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4748
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4748

Query Match 4.8%; Score 113.5; DB 7; Length 336;
Best Local Similarity 26.8%; Pred. No. 0.11;
Matches 55; Conservative 30; Mismatches 30; Indels 43; Gaps 11;

Qy 109 ELDLRDRYLRMPLYDRLHKAESVNDTTAPYK-IKPSDLYTLKXPSHHFKKPHLCV 167
Db 121 QLKAMDGYFNLTMSY-----RSDSDIFTTPYGVLEPWS---GQPAH----- 157
Qy 168 VNDESDPL-----KRGFASVASN--PNAPKNAFVDALNSIEPVTVGGGSKVNTLGVKVN 221
Db 158 -----PPLNLSAKTELVAWAVSNMGPNS-ARVRYYSQSLQAHKLVYGRSHKPL--POGT 209
Qy 222 KNNEFLSQYKFNLCFENSQGYGVVTEKI-IDAVFSHTIPIYMGSPS---VAKDFNPKSFVN 277
Db 210 MMETLSRYKFLAFENSLHDPDITTEKWRNLEAWAVPVVLG-PSRSNYERFLPPDAFIH 268
Qy 278 VHDFKNFDEAIDYVRYLHTHPNAYL 302
Db 269 VDDFQSPKDLARYLQELDKDHARYL 293

RESULT 10
US-10-537-642-6
; Sequence 6, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-6

Query Match 4.8%; Score 112.5; DB 6; Length 1062;
Best Local Similarity 18.9%; Pred. No. 0.68;
Matches 86; Conservative 48; Mismatches 128; Indels 193; Gaps 18;

Qy 145 DSYLTLYTKXPSHHFKKPHLCVAVNDESDPLKRGFASVASNPN-APKRNAPFYDALNSIE 203
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	Query Match	4.7%;	Score 111.5;	DB 7;	Length 2538;	
	Best Local Similarity	19.6%;	Pred. No. 2.9;			
	Matches 113;	Conservative	60;	Mismatches 158;	Indels 245; Gaps 28;	
Qy	8	AFTESASIKQWPLSYPLKLTAVANWVGGAEEFKKSAMYFILSORBYTITLHQNPNEPSDLV	67			
		: : : : :	: :			
Db	1534	ASLPANSFDMPTFKPL	-----EIDASSLAF	-----TNNIAPLDIV	1570	
Qy	68	F-----GSPIGAARKILSYQNTKRVFYAGENEVPNLFDAIGDFELDLR	-----RY	116		
		: : : :	: :			
Db	1571	FETKAKDGRVLGKIKOTLS	---VKRVYNPDE	-----DILFIRETHSGAQ	1612	
Qy	117	LRMPLYDYDRLLH	-----HKASSVNDT	---TAPYKIKPD	-----SLYTLAKK--PSHH	156

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RESULT 12
US-11-070-573-23
; Sequence 23, Application US/11070573
; Publication No. US20060168683A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Cai, Charles
; APPLICANT: Meade, Thomas
; APPLICANT: Moon, Haley
; APPLICANT: Burton, Stephanie
; APPLICANT: Sheets, Joel
; APPLICANT: Merlo, Donald
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins
; FILE REFERENCE: DAS-118XC1
; CURRENT APPLICATION NUMBER: US/11/070,573
; PRIOR FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/549,502
; PRIOR FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: 60/549,516
; PRIOR FILING DATE: 2004-03-02
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 2538
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-11-070-573-23

```

	Query Match	4.7%	Score 111.5;	DB 7;	Length 2538;
	Best Local Similarity	19.6%;	Pred. No. 2.9;		
	Matches 113;	Conservative 60;	Mismatches 158;	Indels 245;	Gaps 28;
Qy	8	AFTESASIKWPLSYPPPLKIAVANNWGGAEEFKKSAFYILSQRYITTLHQNPNEPSDLV	67		
Db	1534	ASLPANSPDMPTFPPL-----EIDASSLAF-----TNNIAPLPLDIV	1570		
Qy	68	F-----GSPIGAARKILSYQNTKRVFYAGENEKVPNLFVDYAIGFDELDRD-----RY	116		
Db	1571	FETKADGRVLGKIKOTLS--VKRWYNAPK-----DILFLRETHSGAQY	1612		

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2458	100.0	78.5	456	9	AEB70149	Hellicobac
2	1929.5	78.5	464	2	AAW86008	Hellicobac	Aeb70149 Hellicobac
3	1929	78.5	476	5	ABG30884	H. pylori	Awb66008 Hellicobac
4	1921.5	78.2	501	5	ABG30881	H. pylori	Abg30884 H. pylori
5	1897	77.2	479	5	ABG30886	H. pylori	Abg30881 H. pylori
6	1897	77.2	485	8	ADJ77814	Hellicobac	Abg30886 H. pylori
7	1897	77.2	485	8	ADJ77814	Hellicobac	Adj77814 Hellicobac
8	1897	77.2	485	9	AEB70135	Hellicobac	Adj77814 Hellicobac
9	1892.5	77.0	486	8	ADJ77810	Hellicobac	Adj77810 Hellicobac
10	1892.5	77.0	486	8	ADJ77810	Hellicobac	Adj77810 Hellicobac
11	1892.5	77.0	486	9	AEB70131	Hellicobac	Adj77810 Hellicobac
12	1889	76.9	454	5	ABG30887	H. pylori	Adj77810 Hellicobac
13	1885.5	76.7	485	5	ABG30882	H. pylori	Adj77810 Hellicobac
14	1817	73.9	432	8	ADJ77812	Hellicobac	Adj77812 Hellicobac
15	1817	73.9	432	8	ADJ77812	Hellicobac	Adj77812 Hellicobac
16	1817	73.9	432	9	AEB70133	Hellicobac	Adj77812 Hellicobac
17	1812.5	73.7	446	9	AEB70145	Hellicobac	Adj77812 Hellicobac
18	1737.5	70.7	440	9	AEB70147	Hellicobac	Adj77812 Hellicobac
19	1722.5	70.1	440	5	ABG30883	H. pylori	Adj77812 Hellicobac
20	1718	69.9	425	8	ADJ77820	Hellicobac	Adj77820 Hellicobac
21	1718	69.9	425	8	ADJ77820	Hellicobac	Adj77820 Hellicobac
22	1718	69.9	425	9	AEB70141	Hellicobac	Adj77820 Hellicobac
23	1712.5	69.7	391	9	AEB70195	H. pylori	Adj77820 Hellicobac

FT Misc-difference 272 /note= "Encoded by AT"
FT Misc-difference 278 /note= "Encoded by GT"
FT Region 465..501
FT /note= "Region not encoded by sequence appearing as
FT ABR89249"
XX US2002068347-A1.
XX 06-JUN-2002.
XX 07-DEC-2000; 2000US-00733524.
XX 05-JUN-1998; 98US-00092315.
XX (UYAL-) UNIV ALBERTA.
XX Taylor DE, Ge Z;
XX WPI; 2002-582480/62.
XX N-PSDB; ABR89249.
XX Purified transmembrane segment-free alphal,3-fucosyltransferase
XX polypeptide useful for producing fucosylated oligosaccharides.
XX Claim 6; Fig 2A; 37pp; English.
XX The invention relates a purified transmembrane segment-free alphas 1,3-
XX fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2-
XX Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
XX Ile, Val or Ala. Also included are the nucleic acid encoding the protein
XX (including its complement or fragment), a vector containing the nucleic
XX acid, a host cell containing nucleic acid or vector, an antibody which
XX selectively binds to the protein and a gene expression system for
XX producing transmembrane segment-free alphas 1,3- fucosyltransferase,
XX comprising a host cell modified with the nucleic acid or its
XX enzymatically active portion. The protein and cells are useful for
XX producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
XX contacting the protein with a substrate such as lacNAc-R and GDP-fucose,
XX and purifying the produced oligosaccharides, or by culturing the cell,
XX contacting the host cell with a substrate, to produce oligosaccharides
XX and purifying the obtained oligosaccharides. The nucleic acid is useful
XX as a probe for detecting the nucleic acid, by contacting a sample with a
XX nucleic acid probe that hybridises to alphas 1,3-fucosyltransferase
XX polynucleotide, and detecting hybridisation of the probe; or by
XX amplifying the nucleic acid using polymerase chain reaction (PCR). The
XX host cell is useful for producing a transmembrane segment-free alphas 1,3-
XX fucosyltransferase-fusion protein, by growing the host cell containing a
XX vector operably linked to a polynucleotide encoding a desired polypeptide
XX or peptide under conditions which allow expression and secretion of the
XX fusion protein and isolating the fusion protein. The antibody is useful
XX for detecting the protein in a sample. The presence of the protein in the
XX sample is indicative of infection by Helicobacter pylori or the presence
XX of malignant cells. The antibody is also useful for diagnosing disorders
XX and monitoring disease, and for inhibiting abnormal alphas 1,3-
XX fucosyltransferase gene product activity. The nucleic acid is useful as
XX part of ribozyme and/or triple helix sequences and for alphas 1,3-
XX fucosyltransferase gene regulation. Oligosaccharides synthesised using
XX the protein or cell are useful in the development of assays to detect
XX mammalian tumours. The present sequence represents H. pylori alphas 1,3
XX fucosyltransferase encoded by the fuct gene
XX Sequence 501 AA;

Query Match 78.2%; Score 1921.5; DB 5; Length 501;
Best Local Similarity 79.1%; Pred. No. 3.9e-156;
Matches 364; Conservative 41; Mismatches 46; Indels 9; Gaps 4;
1 MFQPLDAFIDSTHLDERTHK--PPLVALANWPLKNSEKKGFRDFILHILKQRYII 58
1 MFQPLDAYVESIERKASPPPLKIANVNW--GDEEIKFNSVILISQRYIT 58

QY 59 LHSNPNEPSDLVFCNPLEQARKILSYQNTKRVFTYGENEVFNFLFDYAIQGFDELDFNDR 118
DB 59 LHSNPNEPSDLVFCNPLGSAKILSYQNAKRVFTYGENESFNFLFDYAIQGFDELDFNDR 118
QY 119 YLRMPLYAYLHYKAMLVNDTTSYKUK--ALYTLKPSHFKENHPNLICALIHNESDPW 176
DB 119 YLRMPLYAYLHYKAMLVNDTTSYKUK--ALYTLKPSHFKENHPNLICALIHNESDPW 176
QY 177 KRGFASVFNAPNAPIRNAFYDALNAIEPVASGGSKNTLGVYKVKKNKEFLSQYKFNLCF 236
DB 179 KRGFASVFNAPNAPIRNAFYDALNIEPVVGGSGSVRLTGTNVKKNKEFLSQYKFNLCF 238
QY 237 ENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNNDFAIDYIRYLH 296
DB 239 ENTQGYGVTEKILDAYFSHTPIYQSPSPVAKDFNPKSFVNVHDFNNDFAIDYIRYLH 298
QY 297 AHQNAVYDMLYENPLNTIDGKAGFYQDLSFKILDFPKNILENDTIYHCNDAHYSALHRD 356
DB 299 THKNAYDMLYENPLNTIDGKAGFYQDLSFKILDFPKNILENDTIYHDNPPFC--RD 355
QY 357 LNEPLSVDDLRDHDLDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRDHDLD 416
DB 356 LNEPLSVDDLRDHDLDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLR 415
QY 417 RRDHERLLSKATPILLELSQNTSFKIYRKAYQKSLPLLRAI 456
DB 416 RVNYERLLSKATPILLELSQNTSFKIYRKAYQKSLPLLRAI 455
RESULT 5
ABG30886
ID ABG30886 standard; protein; 479 AA.
XX AC ABG30886;
XX DT 29-AUG-2003 (revised)
XX DT 21-OCT-2002 (first entry)
XX H. pylori alphas 1,3 fucosyltransferase #6.
XX Enzyme; fuct; alphas 1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
XX sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX Helicobacter pylori; strain 763.
XX US2002068347-A1.
XX 06-JUN-2002.
XX 07-DEC-2000; 2000US-00733524.
XX 05-JUN-1998; 98US-00092315.
XX (UYAL-) UNIV ALBERTA.
XX Taylor DE, Ge Z;
XX WPI; 2002-582480/62.
XX Purified transmembrane segment-free alphas 1,3-fucosyltransferase
XX polypeptide useful for producing fucosylated oligosaccharides.
XX Example 3; Fig 6; 37pp; English.
XX The invention relates a purified transmembrane segment-free alphas 1,3-
XX fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2-
XX Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
XX Ile, Val or Ala. Also included are the nucleic acid encoding the protein
XX (including its complement or fragment), a vector containing the nucleic
XX acid, a host cell containing nucleic acid or vector, an antibody which
XX selectively binds to the protein and a gene expression system for
XX producing transmembrane segment-free alphas 1,3- fucosyltransferase,
XX comprising a host cell modified with the nucleic acid or its

enzymatically active portion. The protein and cells are useful for producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by contacting the protein with a substrate such as LacNAc-R and GDP-fucose, and purifying the produced oligosaccharides, or by culturing the cell, contacting the host cell with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alpha1,3-fucosyltransferase polynucleotide, and detecting hybridisation of the probe; or by amplifying the nucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alpha1,3-fucosyltransferase-fusion protein, by growing the host cell containing a vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein and isolating the fusion protein. The antibody is useful for detecting the protein in a sample. The presence of the protein in the sample is indicative of infection by *Helicobacter pylori* or the presence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alpha1,3-fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alpha1,3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an *H. pylori* alpha1,3-fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 479 AA;

Query Match 77.2%; Score 1897; DB 5; Length 479;
Best Local Similarity 76.4%; Pred. No. 4.7e-154;
Matches 363; Conservative 42; Mismatches 46; Indels 24; Gaps 6;

QY 1 MFQPLLDAPIDSTHLDLDE--TTHKPPALVALANWPLKNSKKGFRDPFILHFKLQRYKII 58
DB 1 MFQPLLDAYVESASTEKMAKSPPLKIAVANW--GDEEIEKFNKSVLYFTLSQRYTIT 58

QY 59 LHSNPNESDLVFGNPLEQARKILSYQNTKRVYTGNEVPN--FNLFYAIGFDELDFND 117
DB 59 LHQNPNEFDLVFGNPLGSAKILSYQNAKRVYTTGENESPNEFNLFDYAI GFDELDFND 118

QY 118 RYLRMPLYAYLHYKAMLVNDTTSPLYK--ALYTLKKPSHKPKENHPNLCALIHNESDP 175
DB 119 RYLRMPLYYDRLHKAESVNDTTSPLYKLDNSLYALKPSHCFKPKENLCVAVNDESDP 178

QY 176 WKRGFASPVASNPAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLC 235
DB 179 LKRGFASPVASNPAPIRNAFYDALNSIEPTVGGSVKNTLGYKVKKNNEFTSQYKFNLC 238

QY 236 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDPNPKSFVNVHDFNFDIAIDYRL 295
DB 239 FENTQGYGVVTEKIDAYFSHTIPIYWGSPSVAKDPNPKSFVNVHDFNFDIAIDYIKYL 298

QY 296 HAHONAYLDMLYENPLNTIDGKAGFYQDLSPKILDFKNIILENTIYHCNDAHYSALHR 355
DB 299 HTHKNAYLDMLYENPLNTIDGKAYFYQNLSPKILAFFKTIILENTIYHNDNPFIFC--R 355

QY 356 DLNEPLVSV-----DDLREHDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDD 401
DB 356 DLNEPLVTIDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDD 415

QY 402 LRNVYDDLRLRHDDLRHDLRRHLLSKATPILLELSONTSFKIYRKAYQKSLPLRLAI 456
DB 416 LRNVYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLV 470

RESULT 6

ADJ77814

ID ADJ77814 standard; protein; 485 AA.

XX AC

XX ADJ77814;

XX DT

06-MAY-2004 (first entry)

XX *Helicobacter pylori* strain 1218 FutB protein SeqID 6.
DE FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
XX fucose; N-acetylglucosamine; glycoconjugate; enzyme.
KW *Helicobacter pylori*.
OS
XX WO2004009838-A2.
PN
XX 29-JAN-2004.
PD
XX 23-JUL-2003; 2003WO-US023057.
XX
XX 23-JUL-2002; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
PR
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA
XX Johnson KP, Bezila DJ;
PI
XX WPI; 2004-123401/12.
DR N-PSDB; ADJ77813.
XX
XX New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
XX
XX Claim 16; SEQ ID NO 6; 72pp; English.
XX
XX This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (FutA and FutB) of *Helicobacter pylori* (*H. pylori*). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialylation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an *H. pylori* strain 1218 FutB protein sequence of the invention.
XX
XX Sequence 485 AA;

Query Match 77.2%; Score 1897; DB 8; Length 485;
Best Local Similarity 75.4%; Pred. No. 4.8e-154;
Matches 362; Conservative 41; Mismatches 47; Indels 30; Gaps 5;

QY 1 MFQPLLDAPIDSTHLDLDETHK--PPLNVALANWPLKNSKKGFRDPFILHFKLQRYKII 58
DB 1 MFQPLLDAYIESASIEKITSKSPPLKIAVANW--GDEVEEFPKKNILFYLSQHYTIT 58

QY 59 LHSNPNESDLVFGNPLEQARKILSYQNTKRVYTGNEVPNENLFDYAI GFDELDFND 118
DB 59 LHQNPNEFDLVFGSPIGARKILSYQNAKRVYTTGENESPNEFNLFDYAI GFDELDFR 118

QY 119 YLRMPLYAYLHYKAMLVNDTTSPLYK--ALYTLKKPSHKPKENHPNLCALIHNESDP 176
DB 119 YLRMPLYYDRLHKAESVNDTTSPLYKLDNSLYALKPSHCFKPKENHPNLCVAVNDESDP 178

QY 177 WKRGFASPVASNPAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLCF 236
DB 179 WKRGFASPVASNPAPIRNAFYDALNSIEPTVGGSVKNTLGYKVKKNNEFLSQYKFNLCF 238

QY 237 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDPNPKSFVNVHDFNFDIAIDYRLH 296
DB 239 FENSQGYGVVTEKIDAYFSHTIPIYWGSPSVAKDPNPKSFVNVHDFNFDIAIDYHRYLH 298

QY 297 HAHONAYLDMLYENPLNTIDGKAGFYQDLSPKILDFKNIILENTIYHCNDAHYSALHR 356
DB 299 HTHKNAYLDMLYENPLNTIDGKAYFYQNLSPKILDFKTIILENTIYHNDNPFIFC--YRD 355

[illegible]

RESULT 9	
ADJ77810	
ID	ADJ77810 standard; protein; 486 AA.
XX	
AC	ADJ77810;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Helicobacter pylori strain 1182 FutB protein SegID 2.
XX	
KW	FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KM	fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX	
OS	Helicobacter pylori.
XX	
PN	WO2004009838-A2.
XX	
PD	29-JAN-2004.
XX	
PF	23-JUL-2003; 2003WO-US023057.
XX	
PR	23-JUL-2002; 2002US-0398156P.
PR	08-NOV-2002; 2002US-0424894P.
XX	
PA	(NEOS-) NEOSE TECHNOLOGIES INC.
XX	
PI	Johnson KF, Bezila DJ;
XX	
DR	WPI; 2004-123401/12.
DR	N-PSDB; ADJ77809.
XX	
PT	New isolated polynucleotide encoding fucosyltransferase protein, useful
PT	for synthesizing oligosaccharide moiety on a protein or lipid that is
PT	unglycosylated in its native form or for synthesizing glycolipids.
XX	
PS	Claim 16; SEQ ID NO 2; 72pp; English.
XX	
CC	This invention relates to novel isolated polynucleotides and the encoded
CC	polypeptides thereof, which are related to the fucosyltransferase enzymes
CC	(FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC	refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to

[illegible]

RESULT 10	
ADJ27345	
ID	ADJ27345 standard; protein; 486 AA.
XX	
XX	
AC	ADJ27345;
XX	
DT	20-MAY-2004 (first entry)
XX	
XX	
DE	Alpha-1,3/4-fucosyltransferase.
XX	
XX	
KW	alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
KW	fucosyl; fucose.
XX	
XX	
OS	Helicobacter pylori; strain 1182 FutB.
XX	
XX	
PN	WO2004009793-A2.
XX	
XX	
PD	29-JAN-2004.
XX	
XX	
PF	23-JUL-2003; 2003WO-US023155.

```
XX 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX N-PSDB; ADJ27344.
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX Claim 1; Fig 1; 84pp; English.
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX Sequence 486 AA;
XX Query Match 77.0%; Score 1892.5; DB 8; Length 486;
XX Best Local Similarity 75.1%; Pred. No. 1.2e-153;
XX Matches 361; Conservative 41; Mismatches 48; Indels 31; Gaps 5;
QY 1 MFQPLLDAFIDSTHLDETHK--PPLVALANWPLKNSEKKGRDFILHFLKQRYKII 58
DB 1 MFQPLLDAYIESAIEKITSKSPPLKTIANW--GDEVEEFKKNILYFILSQHYTIT 58
QY 59 LHSNPNEPSDLVFCNPLEQARKILSYQNTKRVFTYTGNEVPNPNLFDYAGFDELDFNDR 118
DB 59 LHQNPNEPSDLVFCSPIGSARKILSYQNAKRVFTYTGNESPNPNLFDYAGFDELDFRDR 118
QY 119 YLRMPLYAYILHYKAMLVNDTTSYKLLK--ALYTLKPKSHKFNHPNLCALIHNESDPW 176
DB 119 YLRMPLYDYRLHKAESVNDTTSYKLLKPDLSYALKKPSHHKFNHPNLCVAVNESDPL 178
QY 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSGVKNTLGYKVKNNKNEFLSQYKFNLCF 236
DB 179 KRGFASVASNPNAPKRNAPFYDVLNSIEPIVGGSGVKNTLGYNIKSEFLSQYKFNLCF 238
QY 237 ENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDPNPKSFVNVDHFNNDFAIDYIRYLH 296
DB 239 ENSQGYGVTEKIIDAYFSHTIPIYWGSPSVQAQDFNPKSFVNVCDKDFDEAIDHVRYLH 298
QY 297 AHQNALDMLYENPLNTIDGKAGFYQDLSEFKILDFPKNILENDTIYHCNDAHYSALHRD 356
DB 299 THPNAYLDMLYENPLNTIDGKAYFYQNLSEFKKILDFFKTILENDTIYHNDPFIF--YRD 355
QY 357 LNEPLVSV-----DGLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 394
DB 356 LNEPLISIDDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 415
QY 395 LRNYDDLVRVNYDDLVRDHDLDLRDHEHLLSKATPLLELSQNTSFKIRKAYQKSLPLL 454
DB 416 LRNYDDLVRVNYDDLVRVNYDDLVRVNYERLQNASPFLLELSQNTTFKIRKAYQKSLPLL 475
QY 455 A 455
DB 476 A 476
```

RESULT 11

AEB70131

ID AEB70131 standard; protein; 486 AA.

```
XX AEB70131;
XX 06-OCT-2005 (first entry)
XX Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 2.
XX Fucosyltransferase; protein production; enzyme.
XX Helicobacter pylori; strain 1182.
XX US2005164338-A1.
XX 28-JUL-2005.
XX 22-JAN-2004; 2004US-00764212.
XX 22-JAN-2004; 2004US-00764212.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
XX (UYAL-) UNIV ALBERTA.
XX Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
XX N-PSDB; AEB70130.
XX New isolated fucosyltransferase polynucleotides and polypeptides, useful
XX for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX Example 1; SEQ ID NO 2; 97pp; English.
XX The present invention provides alpha-1,3/4-fucosyltransferase (also
XX termed as fucosyltransferase) proteins and nucleic acids from various
XX strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
XX fucose residue from a donor substrate to an acceptor substrate. The
XX fucosyltransferase polynucleotides and polypeptides are useful for the
XX synthesis of oligosaccharides, glycoproteins and glycolipids. The present
XX sequence is Helicobacter pylori fucosyltransferase protein.
XX Sequence 486 AA;
XX Query Match 77.0%; Score 1892.5; DB 9; Length 486;
XX Best Local Similarity 75.1%; Pred. No. 1.2e-153;
XX Matches 361; Conservative 41; Mismatches 48; Indels 31; Gaps 5;
QY 1 MFQPLLDAFIDSTHLDETHK--PPLVALANWPLKNSEKKGRDFILHFLKQRYKII 58
DB 1 MFQPLLDAYIESAIEKITSKSPPLKTIANW--GDEVEEFKKNILYFILSQHYTIT 58
QY 59 LHSNPNEPSDLVFCNPLEQARKILSYQNTKRVFTYTGNEVPNPNLFDYAGFDELDFNDR 118
DB 59 LHQNPNEPSDLVFCSPIGSARKILSYQNAKRVFTYTGNESPNPNLFDYAGFDELDFRDR 118
QY 119 YLRMPLYAYILHYKAMLVNDTTSYKLLK--ALYTLKPKSHKFNHPNLCALIHNESDPW 176
DB 119 YLRMPLYDYRLHKAESVNDTTSYKLLKPDLSYALKKPSHHKFNHPNLCVAVNESDPL 178
QY 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSGVKNTLGYKVKNNKNEFLSQYKFNLCF 236
DB 179 KRGFASVASNPNAPKRNAPFYDVLNSIEPIVGGSGVKNTLGYNIKSEFLSQYKFNLCF 238
QY 237 ENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDPNPKSFVNVDHFNNDFAIDYIRYLH 296
DB 239 ENSQGYGVTEKIIDAYFSHTIPIYWGSPSVQAQDFNPKSFVNVCDKDFDEAIDHVRYLH 298
QY 297 AHQNALDMLYENPLNTIDGKAGFYQDLSEFKILDFPKNILENDTIYHCNDAHYSALHRD 356
DB 299 THPNAYLDMLYENPLNTIDGKAYFYQNLSEFKKILDFFKTILENDTIYHNDPFIF--YRD 355
QY 357 LNEPLVSV-----DGLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 394
DB 356 LNEPLISIDDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 415
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PI Taylor DE, Ge Z;
 XX WPI; 2002-582480/62.
 XX Purified transmembrane segment-free alpha,3-fucosyltransferase
 PT polypeptide useful for producing fucosylated oligosaccharides.
 XX Claim 6; Fig 6; 37pp; English.
 XX The invention relates a purified transmembrane segment-free alpha 1,3-
 CC fucosyltransferase polypeptide, having a repeat of the sequence: X1-X2-
 CC fucosyltransferase polypeptide, where X1, X2 and X4 is Asp or Asn; and X3 is
 CC Leu-Arg-X3-X4-Tyr, where X1, X2 and X4 is Asp or Asn; and X3 is
 CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
 CC (including its complement or fragment), a vector containing the nucleic
 CC acid, a host cell containing nucleic acid or vector, an antibody which
 CC selectively binds to the protein and a gene expression system for
 CC producing transmembrane segment-free alpha, 3- fucosyltransferase,
 CC comprising a host cell modified with the nucleic acid or its
 CC enzymatically active portion. The protein and cells are useful for
 CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
 CC contacting the protein with a substrate, such as LachNAC-R and GDP-fucose,
 CC and purifying the produced oligosaccharides, or by culturing the cell,
 CC contacting the host cell with a substrate, to produce oligosaccharides
 CC and purifying the obtained oligosaccharides. The nucleic acid is useful
 CC as a probe for detecting the nucleic acid, by contacting a sample with a
 CC nucleic acid probe that hybridises to alpha,1,3-fucosyltransferase
 CC polynucleotide, and detecting hybridisation of the probe; or by
 CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
 CC host cell is useful for producing a transmembrane segment-free alpha,1,3-
 CC fucosyltransferase-fusion protein, by growing the host cell containing a
 CC vector operably linked to a polynucleotide encoding a desired polypeptide
 CC or peptide under conditions which allow expression and secretion of the
 CC fusion protein and isolating the fusion protein. The antibody is useful
 CC for detecting the protein in a sample. The presence of the protein in the
 CC sample is indicative of infection by Helicobacter pylori or the presence
 CC of malignant cells. The antibody is also useful for diagnosing disorders
 CC and monitoring disease, and for inhibiting abnormal alpha,1,3-
 CC fucosyltransferase gene product activity. The nucleic acid is useful as
 CC part of ribozyme and/or triple helix sequences and for alpha,1,3-
 CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
 CC the protein or cell are useful in the development of assays to detect
 CC mammalian tumours. The present sequence represents an H. pylori alpha,1,3
 CC fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX Sequence 485 AA;
 SQ Query Match 76.7%; Score 1885.5; DB 5; Length 485;
 Best Local Similarity 75.1%; Pred. No. 4.7e-153;
 Matches 361; Conservative 41; Mismatches 48; Indels 31; Gaps 6;
 QY 1 MFQPLDAPIDSTHLDK--PPLNVALANWPLKNSKKGFRDPFILFKQRYKII 58
 DB 1 MFQPLDAPIDSTHLDK--PPLNVALANWPLKNSKKGFRDPFILFKQRYKII 58
 QY 59 LHQNPEDSLVFGNPLEQARKILSYQNTKRVFTGENEVPNFMFLFYAICFDELDNDR 118
 DB 59 LHQNPEDSLVFGNPLEQARKILSYQNTKRVFTGENEVPNFMFLFYAICFDELDNDR 118
 QY 119 YLRMPLYAYLHYKMLVNDTTPSYKLG--ALYTLKPSHKFKENHNLCAIHNESDPW 176
 DB 119 YLRMPLYAYLHYKMLVNDTTPSYKLG--ALYTLKPSHKFKENHNLCAIHNESDPW 176
 QY 177 KRGFASVFNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPN 236
 DB 177 KRGFASVFNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPNAPN 236
 QY 237 ENSQGYGVTEKIDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVDHFNDFEADIDYILH 296
 DB 237 ENSQGYGVTEKIDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVDHFNDFEADIDYILH 296
 QY 297 AHQNAVYDMLYENPLNTIDGKAGFYQNLSPFKKILDFFKTIENDTIYHNDNPFIF 356
 DB 297 AHQNAVYDMLYENPLNTIDGKAGFYQNLSPFKKILDFFKTIENDTIYHNDNPFIF 356
 Db 299 THPNAYVDMLEYENPLNTIDGKAGFYQNLSPFKKILDFFKTIENDTIYHNDNPFIF 355
 QY 357 LNEPLVSV--DRLRRDHDLDLVNVDLRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRL 411
 Db 356 LNEPLVSV--DRLRRDHDLDLVNVDLRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRL 415
 QY 412 -----DHDLDRLDRLHRLSKATPLLELSQNTSPFKIYRKAYQKSLPLLR 454
 Db 416 LRVNYDRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRLVNDLRL 475
 QY 455 A 455
 Db 476 A 476
 RESULT 14
 ADJ77812
 ID ADJ77812 standard; protein; 432 AA.
 AC ADJ77812;
 XX 06-MAY-2004 (first entry)
 DE Helicobacter pylori strain 1111 PutA protein SeqID 4.
 XX PutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
 KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.
 XX Helicobacter pylori.
 XX WO2004009838-A2.
 XX 29-JAN-2004.
 XX 23-JUL-2003; 2003WO-US023057.
 XX 23-JUL-2002; 2002US-0398156P.
 XX 08-NOV-2002; 2002US-0424894P.
 XX (NEOS-) NEOSE TECHNOLOGIES INC.
 XX Johnson KF, Bezila DJ;
 WPI; 2004-123401/12.
 N-PSDB; ADJ77811.
 New isolated polynucleotide encoding fucosyltransferase protein, useful
 for synthesizing oligosaccharide moiety on a protein or lipid that is
 unglycosylated in its native form or for synthesizing glycolipids.
 Claim 16; SEQ ID NO 4; 72pp; English.
 This invention relates to novel isolated polynucleotides and the encoded
 polypeptides thereof, which are related to the fucosyltransferase enzymes
 (PutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
 refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
 chemically synthesise glycoproteins and glycolipids with the desired
 oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
 acetylglucosamine), such that they are useful in the preparation of
 glycoconjugates. The present invention describes how bacterial
 fucosyltransferase is unaffected by the sialylation status of the acceptor
 sugar, as opposed to the mammalian homologue, and furthermore,
 bacterially expressed enzymes offer a large cost saving relative to
 mammalian expression systems. This polypeptide sequence is an H. pylori
 strain 1111 PutA protein sequence of the invention.
 Sequence 432 AA;
 Query Match 73.9%; Score 1817; DB 8; Length 432;
 Best Local Similarity 76.7%; Pred. No. 3.1e-147;
 Matches 352; Conservative 29; Mismatches 42; Indels 36; Gaps 6;
 QY 1 MFQPLDAPIDSTHLDK--PPLNVALANWPLKNSKKGFRDPFILFKQRYKII 59

Result No.	Score	Query Match	Length	DB	ID	Description
1	2005	81.6	454	2	B71914	alpha (1,3)-fucosyltransferase
2	1929	78.5	476	2	C64601	alpha-(1,3)-fucosyltransferase
3	1801.5	73.3	436	2	G71862	alpha-(1,3)-fucosyltransferase
4	1718	69.9	425	2	C64567	hypothetical protein
5	189.5	7.7	346	2	T14327	hypothetical protein
6	189.5	7.7	2657	2	T18497	probable chloroquinase
7	164.5	6.7	2708	2	T09079	alpha-(1,3)-fucosyltransferase
8	157.5	6.4	183	2	C97832	alpha-(1,3)-fucosyltransferase
9	155	6.3	2819	2	T09080	probable chloroquinase
10	147.5	6.0	513	2	F96533	hypothetical protein
11	143.5	5.8	1532	2	T18438	hypothetical protein
12	143	5.8	498	2	D71616	ribosome releasing factor
13	138	5.6	365	2	S55498	alpha (1,3/4)-fucosyltransferase
14	138	5.6	1606	2	T34073	paracetamol - chitinase
15	137.5	5.6	1840	2	T29091	transaminase - chitinase
16	133	5.4	1338	2	T18416	hypothetical protein
17	133	5.4	2500	2	G71609	hypothetical protein
18	131.5	5.3	2269	2	T18472	hypothetical protein
19	130.5	5.3	836	2	T18460	hypothetical protein
20	129.5	5.3	703	2	B34434	arabinoside beta-chitinase
21	128.5	5.2	359	2	A45156	alpha (1,3)-fucosyltransferase
22	128.5	5.2	364	2	T39048	alpha (1,3)-fucosyltransferase
23	127	5.2	789	2	G90587	lipoprotein import
24	126.5	5.1	1652	2	T16799	hypothetical protein
25	125.5	5.1	2013	2	C71610	probable membrane protein
26	124	5.0	525	2	T28306	ORF MSV145
27	124	5.0	653	2	B81277	hypothetical protein
28	123.5	5.0	451	2	T23491	hypothetical protein
29	121.5	4.9	2910	2	T28156	DNA-directed RNA polymerase

[illegible]

QY 419 DHERLLSKATPLELSQNTSFYKRYKAYQKSLPLLRAI 456
Db 414 ---RLQNAPLLELSQNTTFKRYKAYQKSLPLLRIT 448

RESULT 2
C64601
fucosyltransferase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64601
R;Tomb, J.P.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64601
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-476 <TOM>
A;Cross-references: UNIPROT:O25366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID

Query Match 78.5%; Score 1929; DB 2; Length 476;
Best Local Similarity 77.5%; Pred. No. 6.9e-121;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

QY 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYKI 57
Db 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYKI 58

QY 58 ILHNSNPESDLVFGNPLEQARKILSYQNTKRVFTYTGNEVFNPLFDYAIQFDELDFND 117
Db 59 TLHQNPESDLVFGNPLEQARKILSYQNTKRVFTYTGNEVFNPLFDYAIQFDELDFND 118

QY 118 RYLRLMPLYYALHYKAMLVNDTTPSYKLGK--ALYTLAKKPSHKPKENHPLNCALIHNSDP 175
Db 119 RYLRLMPLYYALHYKAMLVNDTTPSYKLGK--ALYTLAKKPSHKPKENHPLNCALIHNSDP 178

QY 176 WKRGFASFVASNAPIRNAPYDALNAIEPVASGSGVKNLTIGYKVKKNNEFLSQYKFNLC 235
Db 179 LKRGFASFVASNAPIRNAPYDALNSIEPVTGGSGVKNLTIGYKVKKNNEFLSQYKFNLC 238

QY 236 FENSQGYGYVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSPVNVHDFNNFDEAIDYIRYL 295
Db 239 FENSQGYGYVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSPVNVHDFNNFDEAIDYIRYL 298

QY 296 HAQONAYLDMLYENPLNTIDGKAGFYQDLSPFKILDPFKNILENDTIYHCHNDHYSALHR 355
Db 299 HTHPENAYLDMLYENPLNTIDGKAGFYQDLSPFKILDPFKNILENDTIYHCHNDHYSALHR 355

QY 356 DLNEPLVSV-----DRLARDHDDLVRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 401
Db 356 DLNEPLVSV-----DRLARDHDDLVRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 415

QY 402 LRNVYDDLRHDDLRLDRHRLSKATPLLELSQNTSFYKRYKAYQKSLPLLRAI 456
Db 416 LRNVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 470

RESULT 3
G71862
alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: G71862

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-436 <ARN>

A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000D36D2; GB:AE001528; GB:AE001439; NID:

A;Experimental source: strain J99

Query Match 73.3%; Score 1801.5; DB 2; Length 436;

Best Local Similarity 75.8%; Pred. No. 1.8e-112;

Matches 350; Conservative 41; Mismatches 42; Indels 41; Gaps 7;

QY 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYK 56

Db 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYK 56

QY 57 ILHNSNPESDLVFGNPLEQARKILSYQNTKRVFTYTGNEVFNPLFDYAIQFDELDFND 116

Db 57 ITLHQNPESDLVFGNPLEQARKILSYQNTKRVFTYTGNEVFNPLFDYAIQFDELDFND 116

QY 117 DRYLRMPLYYALHYKAMLVNDTTPSYKLGK--ALYTLAKKPSHKPKENHPLNCALIHNSD 174

Db 117 DRYLRMPLYYALHYKAMLVNDTTPSYKLGK--ALYTLAKKPSHKPKENHPLNCALIHNSD 176

QY 175 WKRGFASFVASNAPIRNAPYDALNAIEPVASGSGVKNLTIGYKVKKNNEFLSQYKFNLC 234

Db 177 PLKRGFASFVASNAPIRNAPYDALNSIEPVTGGSGVKNLTIGYKVKKNNEFLSQYKFNLC 236

QY 235 CFENSQGYGYVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSPVNVHDFNNFDEAIDYIRY 294

Db 237 CFENTQGYGYVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSPVNVHDFNNFDEAIDYIRY 296

QY 295 LHAQONAYLDMLYENPLNTIDGKAGFYQDLSPFKILDPFKNILENDTIYHCHNDHYSALH 354

Db 297 LHTPENAYLDMLYENPLNTIDGKAGFYQDLSPFKILDPFKNILENDTIYHCHNDHYSALH 353

QY 355 RDLNEPLVSV-----DRLARDHDDLVRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 414

Db 354 RDLNEPLVSV-----DRLARDHDDLVRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 392

QY 415 DLRRDHERLLSKATPLLELSQNTSFYKRYKAYQKSLPLLRAI 456

Db 393 -----RLQNAPLLELSQNTTFKRYKAYQKSLPLLRAI 427

RESULT 4

C64567

fucosyltransferase - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: C64567

R;Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64567
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-425 <TOM>
A;Cross-references: UNIPROT:O25142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID:

Query Match 69.9%; Score 1718; DB 2; Length 425;

Best Local Similarity 72.7%; Pred. No. 6.4e-107;

Matches 335; Conservative 31; Mismatches 45; Indels 50; Gaps 6;

QY 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYKI 57

Db 1 MFQPLLDADFISTHLDTHK---PPLNVALANWPLKNSEKGGFRDFILFHILKQRYKI 58

QY 58 ILHNSNPESDLVFGNPLEQARKILSYQNTKRVFTYTGNEVFNPLFDYAIQFDELDFND 117

[illegible]

Db 302 FNKEDLFILE-HQNIYKKIKEMSTDDQDDVPLI 333

RESULT 7
T09079

probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite (Plasmodium :
C/Species: Plasmodium falciparum
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T09079
F/Su, X.Z.; Kirkman, L.A.; Fujioaka, H.; Wellem, T.E.
Cell 91, 593-603, 1997
A/Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A/Reference number: Z16556; MUID:98054002; PMID:9393853
A/Accession: T09079
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2708 <SUX>
A/Cross-references: UNIPROT:O15791; UNIPARC:UPI0000079A61; EMBL:AF030692; NID:g2642513; M
A/Experimental source: strain 7G8; from Brazil
C/Genetics:
A/Gene: cg2
C/Keywords: toxin resistance

Query Match 6.7%; Score 164.5; DB 2; Length 2708;
Best Local Similarity 21.7%; Pred. No. 0.015;
Matches 114; Conservative 70; Mismatches 173; Indels 169; Gaps 28;

alpha(1,3/4)-fucosyltransferase - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S55498
R/Ouilhouden, A.; Wierinckx, A.; Petit, J.M.; Julien, R.
submitted to the EMBL Data Library, June 1995
A/Description: Molecular cloning and expression of bovine alpha (1,3/4)-fucosyl
A/Reference number: S55498
A/Accession: S55498
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-365 <OUL>

Result No.	Query			DB	ID	Description
	Score	Match	\$			
1	2458	100.0	462	2	Q918S4_HELPU	Q918S4 helicobacte
2	2005	81.6	454	2	Q92LI3_HELPU	Q92LI3 helicobacte
3	1929	78.5	476	2	Q25366_HELPU	Q25366 helicobacte
4	1917.5	78.0	478	2	Q30511_HELPU	Q30511 helicobacte
5	1912	77.8	432	2	Q6ST35_HELPU	Q6ST35 helicobacte
6	1801.5	73.3	436	2	Q92KD7_HELPU	Q92KD7 helicobacte
7	1718	69.9	425	2	Q25142_HELPU	Q25142 helicobacte
8	1452	59.1	333	2	Q32631_HELPU	Q32631 helicobacte
9	460.5	18.7	331	2	Q519S6_BACFN	Q519S6 bacteroides
10	437	17.8	359	2	Q7VPA1_HELPU	Q7VPA1 helicobacte
11	345.5	14.1	287	2	Q21E19_9DSLT	Q21E19 anaeromyxob
12	218	8.9	462	2	Q54PJ9_DICDI	Q54PJ9 dictyosteli
13	200	8.1	600	2	Q50G63_MIMIV	Q50G63 mimivirus.
14	196.5	8.0	389	2	Q54PH9_DICDI	Q54PH9 dictyosteli
15	189.5	7.7	346	2	Q87156_VIBCH	Q87156 vibrio chol
16	189.5	7.7	2870	2	O77380_PLAFA7	O77380 plasmodium
17	189	7.7	818	2	Q55FA8_DICDI	Q55FA8 dictyosteli
18	187.5	7.6	463	2	Q54FK0_DICDI	Q54FK0 dictyosteli
19	187.5	7.6	665	2	Q54L56_DICDI	Q54L56 dictyosteli
20	185	7.5	2359	2	Q81297_PLAFA7	Q81297 plasmodium
21	183.5	7.5	1334	2	O81KL3_PLAFA7	O81KL3 plasmodium
22	179.5	7.3	338	2	O87135_VIBCH	O87135 vibrio chol
23	177.5	7.2	417	2	O86NA8_CTOIN	O86NA8 ciona intes
24	176.5	7.2	338	2	Q34231_VIBCH	Q34231 vibrio chol
25	173.5	7.1	341	2	Q9NFU3_PLAFA	Q9NFU3 plasmodium
26	172.5	7.0	443	2	Q52L0_DROYA	Q52L0 drosophila
27	170.5	6.9	505	2	Q5DTC8_MEDSA	Q5DTC8 medicago sa
28	170.5	6.9	506	2	Q5DTC9_MEDSA	Q5DTC9 medicago sa
29	169.5	6.9	219	2	Q93WS0_MEDTR	Q93WS0 medicago tr
30	169	6.9	359	2	O8UW1_CHICK	O8UW1 gallus gall
31	169	6.9	8094	2	Q81LB9_PLAFA7	Q81LB9 plasmodium

QY T ZT RMPLI I A I H I N A W E V D N D I S F I N T A L I I U N A I I
|||||
|||||

QY T ZT RMPLI I A I H I N A W E V D N D I S F I N T A L I I U N A I I
|||||
|||||

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Db 121 RMPLYAYLHYKAMLVNDTTSPTKYLKALYTLKPKSHKFKENHPNLCALIHNESDPWKRGF 180
Qy 181 ASFVASPNAPIRNAFYDALNAIEPVASGGSVQNTLGYKVKNNKNEFLSOKYKFNLCFENSQ 240
Db 181 RMPLYAYLHYKAMLVNDTTSPTKYLKALYTLKPKSHKFKENHPNLCALIHNESDPWKRGF 180
Qy 241 GYGVTTEKILDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAQN 300
Db 241 GYGVTTEKILDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAQN 300
Qy 301 AYLDMLYENPLNTIDGKAGFYQDLSFKKILDPFKNILENTIYHCNDHAHYSALHRDLNEP 360
Db 301 AYLDMLYENPLNTIDGKAGFYQDLSFKKILDPFKNILENTIYHCNDHAHYSALHRDLNEP 360
Qy 361 LVSVDLRRDHDLDLVNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDL 420
Db 361 LVSVDLRRDHDLDLVNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDL 420
Qy 421 ERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 456
Db 421 ERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 456

RESULT 2
Q9ZLI3_HELPJ
ID Q9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
AC Q9ZLI3_HELPJ
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA (1,3)-FUCOSYLTRANSFERASE.
GN Name=fuct; ORFNames=jhp 0596;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
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CC -----
DR EMBL; AE001439; AAD06169.1; -; Genomic_DNA.
DR PIR; B71914; B71914.
DR BIOCyc; HPYL85963:JHP0596-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 454 AA; 53448 MW; 3262697131263AB0 CRC64;

Query Match 81.6%; Score 2005; DB 2; Length 454;
Best Local Similarity 82.3%; Pred. No. 1.1e-123;
Matches 377; Conservative 30; Mismatches 39; Indels 12; Gaps 3;

Qy 1 MFQPLLDADISTHLDTHPPNVALANWPLKNSEKGFDPILFHLKQRYKIILH 60
Db 1 MFQPLLDADISTHLDTHPPNVALANWPLKNSEKGFDPILFHLKQRYKIILH 60
Qy 61 SNPNPESDLVFGSPIGSARKILSYQNTKRVFTGNEVPNPNLFDAIGFDELDFRDYL 120

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Db 61 QNPNEPSDLVFGSPIGSARKILSYQNTKRVFTGNEVPNPNLFDAIGFDELDFRDYL 120
Qy 121 RMPLYAYLHYKAMLVNDTTSPTKYLK--ALYTLKPKSHKFKENHPNLCALIHNESDPWKR 178
Db 121 RMPLYAYLHYKAMLVNDTTSPTKYLK--ALYTLKPKSHKFKENHPNLCALIHNESDPWKR 178
Qy 179 GFASFVASPNAPIRNAFYDALNAIEPVASGGSVQNTLGYKVKNNKNEFLSOKYKFNLCFEN 238
Db 181 GFASFVASPNAPIRNAFYDALNSIEPTVGGSGVQNTLGYKVKNNKSEPLSOKYKFNLCFEN 240
Qy 239 SQGYVTEKILDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAH 298
Db 241 TQGYVTEKILDAYFSHTPIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 300
Qy 299 QNAVLDMLYENPLNTIDGKAGFYQDLSFKKILDPFKNILENTIYHCNDHAHYSALHRDLN 358
Db 301 PNAVLDMLYENPLNTIDGKAYFYQNLSPKILDPFKNILENTIYHNPFFI---YRDLN 357
Qy 359 EPLVSVDDLRRDHDLDLVNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDL 418
Db 358 EPLVAIDDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVDLRYNVD 413
Qy 419 DHERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 456
Db 414 ---RLQNASPLLESQNTSFKIYKAYOKSLPLLRTI 448

RESULT 3
O25366_HELPJ
ID O25366_HELPJ PRELIMINARY; PRT; 476 AA.
AC O25366_HELPJ
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Fucosyltransferase.
GN Ordered locus Names=HP0651; ORFNames=HP 0651;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=26695 / ATCC 700392;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Fujii C., Bowman C.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
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CC -----
DR EMBL; AE000511; AAD07710.1; -; Genomic_DNA.
DR PIR; C64601; C64601.
DR TIGR; HP0651; -.
DR LinkHub; O25366; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 476 AA; 55927 MW; 32BFFDBBD36E1F74 CRC64;

```

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Query Match      78.5%; Score 1929; DB 2; Length 476;
Best Local Similarity 77.5%; Pred. No. 1.1e-118;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

QY 1 MFQPLDAPIDSTHLDTHK---PPLNVALANWPLKNSKKGPRDFILHILKQRYKI 57
DB 1 MFQPLDAPIDSTHLDTHK---PPLNVALANWPLKNSKKGPRDFILHILKQRYKI 58
QY 58 ILHSPNPSDLVFGNPLEQARKILSYQNTKRVFTYGENEVNPNLFDYAIGFDELDFND 117
DB 59 TLHQPNRESSDLVFSNPLGAARKILSYQNTKRVFTYGENEVNPNLFDYAIGFDELDFND 118
QY 118 RYLMPLYYAYLHYKAMLVNDTTSYKLGK--ALYTLKPSHKPKENHNPNCALIHNSDP 175
DB 119 RYLMPLYYAYLHYKAMLVNDTTSYKLGK--ALYTLKPSHKPKENHNPNCALIHNSDP 176
QY 176 WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVNTLGYKVNKNEFLSQYKFNLC 235
DB 179 LKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVNTLGYKVNKNEFLSQYKFNLC 238
QY 236 FENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDFAIDYIRYL 295
DB 239 FENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDFAIDYIRYL 298
QY 296 HAHQNAVYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNIILENDTIYHCNDHAHYSALHR 355
DB 299 HTHPNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNIILENDTIYHNPFPF---YR 355
QY 356 DLNEPLVSV-----DDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 401
DB 356 DLNEPLVSV-----DDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 415
QY 402 LRVNYDDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 456
DB 416 LRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 470

RESULT 4
O30511_HELPY PRELIMINARY; PRT; 478 AA.
AC Q30511;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Alpha-1,3-fucosyltransferase.
GN Name=fucT;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTCT 11639;
RX MEDLINE=97407925; PubMed=92611149; DOI=10.1074/jbc.272.34.21357;
RA Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.;
RT "Cloning and heterologous expression of an alpha1,3-fucosyltransferase
RL gene from the gastric pathogen Helicobacter pylori.";
RL J. Biol. Chem. 272:21357-21363(1997).
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CC -----
DR EMBL; AF008596; AAB81031.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;
```

Query Match

78.0%; Score 1917.5; DB 2; Length 478;

```
Best Local Similarity 77.0%; Pred. No. 6.5e-118;
Matches 365; Conservative 41; Mismatches 45; Indels 23; Gaps 5;

QY 1 MFQPLDAPIDSTHLDTHK---PPLNVALANWPLKNSKKGPRDFILHILKQRYKI 58
DB 1 MFQPLDAPIDSTHLDTHK---PPLNVALANWPLKNSKKGPRDFILHILKQRYKI 58
QY 59 LHSNPNPSDLVFGNPLEQARKILSYQNTKRVFTYGENEVNPNLFDYAIGFDELDFND 118
DB 59 LHSNPNPSDLVFGNPLEQARKILSYQNTKRVFTYGENEVNPNLFDYAIGFDELDFND 118
QY 119 RYLMPLYYAYLHYKAMLVNDTTSYKLGK--ALYTLKPSHKPKENHNPNCALIHNSDP 176
DB 119 RYLMPLYYAYLHYKAMLVNDTTSYKLGK--ALYTLKPSHKPKENHNPNCALIHNSDP 178
QY 177 KRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVNTLGYKVNKNEFLSQYKFNLC 236
DB 179 KRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVNTLGYKVNKNEFLSQYKFNLC 238
QY 237 FENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDFAIDYIRYL 296
DB 239 FENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDFAIDYIRYL 298
QY 297 HAHQNAVYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNIILENDTIYHCNDHAHYSALHR 356
DB 299 HTHPNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNIILENDTIYHNPFPF---YR 355
QY 357 DLNEPLVSV-----DDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 402
DB 356 DLNEPLVSV-----DDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 415
QY 403 LRVNYDDLRRDHDLDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 456
DB 416 LRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 469

RESULT 5
O6ST35_HELPY PRELIMINARY; PRT; 432 AA.
AC Q6ST35;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Alpha-1,4-fucosyltransferase.
GN Name=fucTII;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 6709;
RX PubMed=16000696; DOI=10.1093/glycob/cwj004;
RA Rabbani S., Miksa V., Wipf B., Ernst B.;
RT "Molecular Cloning and Functional Expression of a Novel Helicobacter
RT pylori (alpha)-1,4 Fucosyltransferase.";
RL Glycobiology 15:1076-1083(2005).
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CC -----
DR EMBL; AY450598; AAR88243.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;
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Query Match

77.8%; Score 1912; DB 2; Length 432;

Matches 359; Conservative 32; Mismatches 33; Indels 34; Gaps 4;

QY 1 MFQPLDADFIDSTHLDTHKPPPLVALANWPLKNSKKGFRDFILHFIKQRYKILH 60
 DB 1 MFQPLDADFIDSTHLDTHKPPPLVALANWPLKNSKKGFRDFILHFIKQRYKILH 56
 QY 61 SNPNESDLVFGNPLEOARKILSYQNTKRVFYTGNEVPNPNFLFDYAIGFDELDFNDRL 120
 DB 57 RNPDKPADIVFGNPLEOARKILSYQNTKRVFYTGNEVPNPNFLFDYAIGFDELDFNDRL 116
 QY 121 RMPLYYAYLHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLCALIHNESDPWKR 178
 DB 117 RMPLYYAYLHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLCALIHNESDPWKR 176
 QY 179 GFASFVSNAPNAPIRNAPYDALNAIEBPVAGSGSVKNTLGYKVKNEFLSQYKFNLCFEN 238
 DB 177 GFASFVSNAPNAPIRNAPYDALNAIEBPVAGSGSVKNTLGYKVKNEFLSQYKFNLCFEN 236
 QY 239 SQGVGYVTEKILDAYFSHHTPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDYRLYLAH 298
 DB 237 SQGVGYVTEKILDAYFSHHTPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDYRLYLAH 296
 QY 299 QNAYLDMYENPLNTIDGKAGFYQDLSEFKILDFFKNILENDTIYHCNDAHYSALHRLN 358
 DB 297 QNAYLDMYENPLNTIDGKAGFYQDLSEFKILDFFKNILENDTIYHCNDAHYSALHRLN 356
 QY 359 EPLVSDLLRRDHDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVNVDL 418
 DB 357 EPLVSI-----DOLRINYDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVNVDL 390
 QY 419 DHERLSKATPPLLELSQNTSPKIYRKAYOKSLPLLR 456
 DB 391 --ERLQNASPPLLELSQNTSPKIYRKAYOKSLPLLR 426

RESULT 6

Q9ZKD7_HELPJ
 ID Q9ZKD7_HELPJ PRELIMINARY; PRT; 436 AA.
 AC Q9ZKD7_HELPJ
 DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999, sequence version 1.
 DT 21-FEB-2006, entry version 23.
 DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.
 GN Name=fuc0; ORFNames=jhp_1002;
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
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 CC -----
 CC ENMBL; AE001439; AAD06573.1; -; Genomic_DNA.
 DR PIR; G71862.
 DR GO; GO:016020; C:membrane; IEA.
 DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro; IPR001503; Glyco trans 10.
 DR PANTHER; PTHR01929; Glyco trans 10; 1.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 436 AA; 50699 MW; 1DB2066AE98FA61E CRC64;

Query Match 73.3%; Score 1801.5; DB 2; Length 436;
 Best Local Similarity 75.8%; Pred. No. 2.5e-110;
 Matches 350; Conservative 30; Mismatches 41; Indels 41; Gaps 7;

QY 1 MFQPLDADFIDSTHLDTHK--PPLVALANWPLKNSKKGFRDFILHFIKQRYK 56
 DB 1 MFQPLDADFIDSTHLDTHKPPPLKIAVANW-----CGAEFKKSTLYFILSQRYT 56
 QY 57 IILHSNPNESDLVFGNPLEOARKILSYQNTKRVFYTGNEVPNPNFLFDYAIGFDELDFN 116
 DB 57 IILHSNPNESDLVFGNPLEOARKILSYQNTKRVFYTGNEVPNPNFLFDYAIGFDELDFN 116
 QY 117 DRYLRMPLYYAYLHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLCALIHNESD 174
 DB 117 DRYLRMPLYYAYLHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLCALIHNESD 176
 QY 175 PWKRGFASFVSNAPNAPIRNAPYDALNAIEBPVAGSGSVKNTLGYKVKNEFLSQYKFN 234
 DB 177 PLKRGFASFVSNAPNAPIRNAPYDALNSIEPVTGGSVKNTLGYNVKNKSEFLSQYKFN 236
 QY 235 CFENSGQGVYVTEKILDAYFSHHTPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDYRY 294
 DB 237 CFENSGQGVYVTEKILDAYFSHHTPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDYRY 296
 QY 295 LHAHONAYLDMYENPLNTIDGKAGFYQDLSEFKILDFFKNILENDTIYHCNDAHYSALH 354
 DB 297 LHTHPNAYLDMYENPLNTIDGKAGFYQDLSEFKILDFFKNILENDTIYHCNDAHYSALH 353
 QY 355 RDLNEPLVSDLLRRDHDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVN 414
 DB 354 RDLNEPLVSI-----DOLRINYDLDLVNVDLAVNTDLDLVNVDLAVNTDLDLVN 392
 QY 415 DLRDHERLSKATPPLLELSQNTSPKIYRKAYOKSLPLLR 456
 DB 393 -----RLQNASPPLLELSQNTSPKIYRKAYOKSLPLLR 427

RESULT 7
 O25142_HELPY
 ID O25142_HELPY PRELIMINARY; PRT; 425 AA.
 AC O25142_HELPY
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Fucosyltransferase.
 GN OrderedLocusNames=HP0379; ORFNames=HP_0379;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX STRAIN=26695 / ATCC 700392;
 RA Fleisigmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
 RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori.";
 RL Nature 388:539-547(1997).
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 CC -----
 CC ENMBL; AE000511; AAD07447.1; -; Genomic_DNA.
 DR PIR; C64567; C64567.

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DR TIGR; HP0379; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;

Query Match 69.9%; Score 1718; DB 2; Length 425;
Best Local Similarity 72.7%; Pred. No. 7.7e-105;
Matches 335; Conservative 31; Mismatches 45; Indels 50; Gaps 6;

QY 1 MFQELLDFAIDSTHLDTHK---PPLNVALANWNNPLKNSEKKGRDFTLHILKQRYKI 57
DB 1 MFQELLDFAIESASIEKMASKPPPLKIANWNN--GDEEKEFKSVLYFILSORVAI 58

QY 58 ILHGNPNESDLPFGNPLEQARKILSYQNTKRVFTYGENEVNPNLFDYAIQFDELDFND 117
DB 59 TLHQNPNEFSLVFSNPLGAARKILSYQNTKRVFTYGENESPNFLFDYAIQFDELDFND 118

QY 118 RYLEMPLYAYLHYKAMLVNDTTSYKLG--ALYTLKPSHKFKENHPNLCALIHNESDP 175
DB 119 RYLEMPLYAYLHYKAEIVNDTTPAYKLGKNSLYALKKPSHHFKENHPNLCVAVNDESD 178

QY 176 WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKNEFLSYQKFNLC 235
DB 179 LKRGFASVASNAPMNAFYNALNSIEPTVGGSVRNTLGYKVGKSEFLSYQKFNLC 238

QY 236 FENSGQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYRYL 295
DB 239 FENSGQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYRYL 298

QY 296 HAHQNAVLDMLYENPLNTIDGKAGFYQDLSEFKILDPPKNILENTIYHCNDAHYSALHR 355
DB 299 HTHPNAVLDMLYENPLNTIDGKAGFYQDLSPFKILDFFKTLILENTIYHKSTSP--MWEY 357

QY 356 DLNEPLYSVDLRRDHDHDLRVNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYDDLRRDHD 415
DB 358 DLHKPLVSI-----DGLRVNYDDLVRNYD----- 381

QY 416 LRRDHERLSKATPLLELSQNTSPKIRKAYOKSLPLLRAI 456
DB 382 -----RLQNASPLLELSQNTSPKIRKAYOKSLPLLRV 416

RESULT 8
O32631_HELPY PRELIMINARY; PRT; 333 AA.
AC O32631;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DE Alpha-(1-3)-fucosyltransferase (EC 2.4.1.-).
GN Name=fuct;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11637;
RX MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Bijnden D.H.,
RA Bird M.I.;
RT "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
RT alpha(1,3)-fucosyltransferase gene.";
RL J. Biol. Chem. 272:21349-21356(1997).
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DR EMBL; AF006039; AAB93985.1; --; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFFCB1AC127E0A8C CRC64;

Query Match 59.1%; Score 1452; DB 2; Length 333;
Best Local Similarity 81.6%; Pred. No. 1.9e-87;
Matches 275; Conservative 26; Mismatches 24; Indels 12; Gaps 3;

QY 122 MPLYAYLHYKAMLVNDTTSYKLG--ALYTLKPSHKFKENHPNLCALIHNESDPKRG 179
DB 1 MPLYAYLHYKAMLVNDTTSYKLG--ALYTLKPSHKFKENHPNLCALIHNESDPKRG 60

QY 180 FASFVASNPAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKNEFLSYQKFNLCFENS 239
DB 61 FASFVASNPAPMNAFYNALNSIEPTVGGAVKNTLGYKVGKSEFLSYQKFNLCFENS 120

QY 240 QGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYRYLHAQ 299
DB 121 QGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYRYLTHP 180

QY 300 NAYLDMLYENPLNTIDGKAGFYQDLSEFKILDPPKNILENTIYHCNDAHYSALHRDLE 359
DB 181 NAYLDMLYENPLNTIDGKAGFYQDLSEFKILDPPKNILENTIYHNPFFI---YRDLE 237

QY 360 PLVSVDDLRRDHDHDLRVNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYDDLRRDHDHDLRRD 419
DB 238 PLVSI-----DNLRVNYDDLVRNYDDLVRNYDDLVRNYDDLVRNYDDLRRDHDHDLRRD 290

QY 420 HERRLSKATPLLELSQNTSPKIRKAYOKSLPLLRAI 456
DB 291 YERLLQNASPLLELSQNTSPKIRKAYOKSLPLLRVI 327

RESULT 9
QSL9S6_BACFN PRELIMINARY; PRT; 331 AA.
AC QSL9S6;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DE Putative LPS biosynthesis related glycosyltransferase.
GN OrderedLocusNames=BF3460;
OC Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Foxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RT Science 307:1463-1465(2005).
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QY 132 KAMLVNDTTPYKLYKALYTLKPKSHKFKENHPNLCALIHNESDPWKRGFASFVSNPNAP 191
 Db 100 PRFL-----ERRDVNAIVAB-----KTRFCNLVCSNRAAR 131
 QY 192 IRNAPYDALNAIEPVASGGSVKNTLGYKVKKNKNEFLSQYKFNLCFENSOGYGYVTEKILD 251
 Db 132 ERLAPFEKLSRYKPPDSGGRVNNVGGPVOKLAFIRQHRFTIAFENASYPGYTTEKIVE 191
 QY 252 AYFSHTIDYVSGSPVADFNPKSPVNVDFNFDNDEADYIRYLHAHQNALYMLYENPL 311
 Db 192 PMRVGSIPIYGNLVLHLDPLRSIVSWHEGSDAAIERVQIDRDELYRHMLLQPF 251
 QY 312 NTIDKAGFYQDLSPEKIDFFKNTLENTIYHCNDHVSALHRLNRP 360
 Db 252 P--EGRPYPSDPGV--LLDWLERV-----FSTPRDRARP 283

RESULT 12
 Q54PJ9_DICDI PRELIMINARY; PRT; 462 AA.
 AC Q54PJ9;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 07-MAR-2006, entry version 5.
 DE Hypothetical protein.
 GN ORFNames=DD80186041;
 OS Dictyostelium discoideum (slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RX PubMed=15975012; DOI=10.1038/nature03481;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
 RA Sugrang B., Berriaman M., Song J., Olsen R., Szafarski K., Xu Q.,
 RA Tunggal R., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Filcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
 RA Kierhornou A., Nle X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Church C.M.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
 RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
 RA Knights A., Loulsegged H., Mungall K.L., Oliver K., Price C.,
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitz E., Steffen D.,
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
 RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
 RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
 RA Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 435:43-57(2005).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC EMBL; AAT101000108; EAL65179.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro; IPR001503; Glyco_trans_10.
 DR PANTHER; PTHR11929; Glyco_trans_10; 1.
 KW Glycosyltransferase; Golgi stack; Hypothetical protein; Transferase;
 KW Transmembrane.
 SQ SEQUENCE 462 AA; 54815 MW; 444843FFBAEF6D77 CRC64;

Query Match 8.9%; Score 218; DB 2; Length 462;

Best Local Similarity 24.9%; Pred. No. 5e-06;
 Matches 85; Conservative 53; Mismatches 126; Indels 78; Gaps 15;
 QY 40 KGFROPILHFKQRYKIILHNSPNSDLVFCN-----PLEQARKILLSYQNTKRVFTYGE 95
 Db 124 KGLDDKFFYIVRPPY-----PNQKLDNEIWSYDIIVDFEAPKKKLSRRVPRTLSME 176
 QY 96 NEVPN-----FNLFDYAIGFDELDFNDRLRM-----PLYAYLHYKAMLVNDT-- 140
 Db 177 PQ-PNRTCEFDKCEFFNFNKSFE-----SQSDIRMGFDTPSSSAYKLYNKLITIDEIAKI 231
 QY 141 -SPYKLYKALYTLKSHKFKENHPNLCALIHNESDPWKRGFASFVSNPNAPINAFDA 199
 Db 232 QTQFKLE--YQWKNNTLQP-----HOKSIPLANWFCTNCNHSN---RNEYVOE 277
 QY 200 INAIPEVAS-GGSVKNT-----LGKVKKNKNEFLSQYKFNLCFENSOGYGYVTEKI 249
 Db 278 LMKFIVVDSFGKLNKMPSTNFSLGSQDFFERKRLFITRYKFTIVFENSICKDYVSEKV 337
 QY 250 LDAYFSHTIPIYWGSPSVAKDFNPKSFVNVVDFNPNFDEADYIRYLHAHQNALYML-LYE 308
 Db 338 LDALLTAGSVPIFWGHPSTIKYLPILNSYIFVGFQKNAHLNHLKFLSENDNEYFKLHTWR 397
 QY 309 NPLNTID-----GKAGP-----YQDLSFEKI 329
 Db 398 TNQTVIDQWGVNYPNPKGFRFRVQCPILRHYQLKTKGI 439

RESULT 13
 Q5UO63_MIMIV PRELIMINARY; PRT; 600 AA.
 AC Q5UO63;
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-DEC-2004, sequence version 1.
 DE Hypothetical protein.
 GN ORFNames=MIMI_R654;
 OS Mimivirus.
 OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
 OX NCBI_TaxID=212035;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Rowbotham-Bradford;
 RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
 RA La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
 RA Drancourt M., Birtles R., Claverie J.M., Raoult D.;
 RT "A giant virus in amoebae.";
 RL Science 299:2033-2033(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Rowbotham-Bradford;
 RX PubMed=15486256; DOI=10.1126/science.1101485;
 RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
 RA La Scola B., Susan M., Claverie J.-M.;
 RT "The 1.2-megabase genome sequence of Mimivirus.";
 RL Science 306:1344-1350(2004).
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 CC EMBL; AY653733; AAV50915.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro; IPR001503; Glyco_trans_10.
 DR PANTHER; PTHR11929; Glyco_trans_10; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 600 AA; 70731 MW; 123F17F7591E9DD9 CRC64;

Query Match 8.1%; Score 200; DB 2; Length 600;
 Best Local Similarity 21.6%; Pred. No. 0.0001;
 Matches 68; Conservative 62; Mismatches 109; Indels 76; Gaps 13;

QY 36 NSBKGGFDFILFK--ORYKIILHSNPNPSPDLVGNPLEQARKILSYQNTKRVFT 93
DB 319 NDAKYSWHLVAVLKFIPYKLV---GPTDNDVISINHLVEQ---FIRPDSFNILIT 372
QY 94 GENEVPNPNFLDYAIGDELDNDRYL---RMPLYAYL-----HYKAMLVNDTTSPPYK 144
DB 373 GEPTM-NITVDMCI-----DTKYTSQSSITVYPIFPSSMRHRKSLNHTDYI----- 420
QY 145 LKALYTLKPSHKFKENHPNLCALIHNSDPWKGFPASFPVSNPNAPIRNAFYDALNAIE 204
DB 421 -----KPTKTF-----CAYMNMRYPHRIWYFNLSK-----YRQVDALG 455
QY 205 PVASGGSVKMTLGVKVNKN-----EFLSQYKFNLCFNSQGGYGYVTEKILDAYFSHTI 258
DB 456 KCCNVVDIKDSRSHFTSESTYNDIAIELYSEYKFLVALENIWPGYSTEKILNPMIANSI 515
QY 259 PIYWGSPSVAKDPNPKSFVNVDHFNPNFDEAIDYIRYLHAHQNAFLDM-----LYENPLNTI 314
DB 516 PIYWGSDTIKHNKKTIVIPDPNPTDLEHKNIDTNDLYKSIINPEIYNP----- 571
QY 315 DGKAGFYQDLSPEKI 329
DB 572 -----DFSLDKL 578

RESULT 14
Q54PH9_DICDI PRELIMINARY; PRT; 389 AA.
AC Q54PH9;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Hypothetical protein fut1.
GN Names=fut1; ORFNames=DB0219943;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggul A.T., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Parbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindbay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulsegged H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.P., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AAFI01000108; EAL65160.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; P:fucosyltransferase activity; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.

DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Golgi stack; Hypothetical protein; Transferase;
KW Transmembrane.
SQ SEQUENCE 389 AA; 45383 MW; 9EA7D88C3D423F99 CRC64;
Query Match 8.0%; Score 196.5; DB 2; Length 389;
Best Local Similarity 23.9%; Pred. No. 0.00011;
Matches 80; Conservative 57; Mismatches 111; Indels 87; Gaps 17;
QY 52 KORYKIILHSN-PNEPSP-----LVFGNPLEQARKILSYQNTKRVF----- 91
DB 65 KFKCKIBIHSFSEKAEQAIIYFFSQYQSSNKI--YNNTLKRYNPRQITIGWTMES 122
QY 92 -----YTGNE--VPNENLFDYAIGDEL-DFNDR-VLRMPLYAYLHYKAMLVNDTTS 142
DB 123 GGLYRFSGDSNFIISNFI---TVGYPRVDFNFKQTHIYVP--YGPVEYSG-----SDS 171
QY 143 YKLKALYTLKK--PSHKFKENHPNLCALIHNSDPWKGFPASFPVSNPNAPIRNAFYDAL 200
DB 172 YAHSAKFDRIKEIPS---KRNN---SIVWISSNCWHEDYK-----RVYLMRSI 213
QY 201 NAIEPVASGGSVKMTLGY-----KVKKNFELSQYKFNLCFNSQGYGVTEKILD 251
DB 214 MNITKVDYSGLNNIDFTDQDKLINSKHDQMDVLYKRYNFAIFENSCLKDYITEKLWE 273
QY 252 AYFSHTIPIYWGSPSVAKDP-NPKSFVNVDHFNPNFDEAIDYIRYLHAHQNAFLDM----- 306
DB 274 SLSVGTIPIYLGAPNIMEFLPDPDSIINVRPKSVNDLVDIYIKKVENDDQNLRLKHLKWIK 333
QY 307 -----YENPLNTIDGKAGFYQDLSPEKIL 330
DB 334 IKKWSKEFQNIYDESNNLDPLCSICSISKIASKIL 368

RESULT 15
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AC O87156;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Wbfl protein.
GN Name=wbfl;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O22;
RX MEDLINE=99453293; PubMed=10521656; DOI=10.1016/S0378-1119(99)00344-3;
RA Yamasaki S., Shimizu T., Hoshino K., Ho S.-T., Shimada T., Nair G.B.,
RA Takeda Y.;
RT "The genes responsible for O-antigen synthesis of Vibrio cholerae O139
are closely related to those of Vibrio cholerae O22.";
RL Gene 237:321-332(1999).
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AB012957; BAA33631.1; -; Genomic_DNA.
DR PIR; T44327; T44327.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; P:fucosyltransferase activity; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
SQ SEQUENCE 346 AA; 40359 MW; 28690BC3FFEFDA7F CRC64;
Query Match 7.7%; Score 189.5; DB 2; Length 346;
Best Local Similarity 23.3%; Pred. No. 0.00027;
Matches 72; Conservative 65; Mismatches 85; Indels 87; Gaps 18;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:45:14 ; Search time 31.2608 Seconds
(without alignments)
1276.805 Million cell updates/sec

Title: US-10-764-212-20

Perfect score: 2458

Sequence: 1 MFQPLLDADFIDSTHLDETH.....TSFKYRKAYQKSLPLRAI 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pbp:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pbp:*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pbp:*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1934.5	78.7	464	2	US-09-092-315-1 Sequence 1, Appli
2	1934.5	78.7	464	2	US-09-733-524A-1 Sequence 1, Appli
3	1934.5	78.7	464	2	US-10-189-977A-1 Sequence 1, Appli
4	1934.5	78.7	464	3	US-10-392-098A-1 Sequence 1, Appli
5	1929	78.5	476	2	US-09-092-315-5 Sequence 5, Appli
6	1929	78.5	476	2	US-09-733-524A-5 Sequence 5, Appli
7	1929	78.5	476	2	US-10-189-977A-5 Sequence 5, Appli
8	1929	78.5	476	3	US-10-392-098A-5 Sequence 5, Appli
9	1925.5	78.3	478	2	US-09-092-315-7 Sequence 7, Appli
10	1917.5	78.0	478	2	US-09-733-524A-7 Sequence 7, Appli
11	1917.5	78.0	478	2	US-10-189-977A-7 Sequence 7, Appli
12	1917.5	78.0	478	3	US-10-392-098A-7 Sequence 7, Appli
13	1892.5	77.0	486	2	US-09-092-315-2 Sequence 2, Appli
14	1892.5	77.0	486	2	US-09-733-524A-2 Sequence 2, Appli
15	1892.5	77.0	486	2	US-10-189-977A-2 Sequence 2, Appli
16	1892.5	77.0	486	3	US-10-392-098A-2 Sequence 2, Appli
17	1889	76.9	454	2	US-09-092-315-8 Sequence 8, Appli
18	1889	76.9	454	2	US-09-733-524A-8 Sequence 8, Appli
19	1889	76.9	454	2	US-10-189-977A-8 Sequence 8, Appli
20	1889	76.9	454	3	US-10-392-098A-8 Sequence 8, Appli
21	1737.5	70.7	440	2	US-09-092-315-3 Sequence 3, Appli
22	1737.5	70.7	440	2	US-09-733-524A-3 Sequence 3, Appli
23	1737.5	70.7	440	2	US-10-189-977A-3 Sequence 3, Appli
24	1737.5	70.7	440	3	US-10-392-098A-3 Sequence 3, Appli
25	1718	69.9	425	2	US-09-092-315-6 Sequence 6, Appli
26	1718	69.9	425	2	US-09-733-524A-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-092-315-1

; Sequence 1, Application US/09092315

; Patent No. 6399337

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE

; FILE REFERENCE: 07254/049001

; CURRENT APPLICATION NUMBER: US/09/092,315

; CURRENT FILING DATE: 1998-06-05

; EARLIER APPLICATION NUMBER: US 60/048,857

; EARLIER FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-09-092-315-1

Query Match 78.7%; Score 1934.5; DB 2; Length 464;

Best Local Similarity 79.3%; Pred. No. 4.9e-180;

Matches 365; Conservative 41; Mismatches 45; Indels 9; Gaps 4;

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QY	59	LHSNPNPSDLVFGNPLEQARKILSYQNTKRVYTTGENEVPNPNLFDYAIGFDELDFNDR	118
DB	59	LHQNPNESDLVFGNPLGSARKILSYQNAKRVFYTGENSEPNPNLFDYAIGFDELDFNDR	118
QY	119	YLRLMPLYAYLHYKAMLVNDTTSYKLGK--ALYTKKPSHKPKENHPNLICALIHNSDPW	176
DB	119	YLRLMPLYDYRLHHAESVNDTTPAYKLIKNSLYALKKPSHKPKENHPNLCAVVNDSDDL	178
QY	177	KRGFASFVSNPNADIRNAFYDAINAEIPEVSGSVKNTLGYKVNKNKNEFLSOYKKNLCF	236
DB	179	KRGFASFVSNPNADIRNAFYDALNSIEPVTGGSVRNTLGYNVKNKNKNEFLSOYKKNLCF	238
QY	237	ENSOQGVYVTEKILDAYFSHTIPIYWGSPSVAKDNPNSFVNVDNFNNDEADIDYIRYLH	296
DB	239	ENTQGVYVTEKILDAYFSHTIPIYWGSPSVAKDNPNSFVNVDNFNNDEADIDYIRYLH	298
QY	297	AFQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFPKNILENTDIYHCNDAHYSALHRD	356
DB	299	THKNAYLDMLYENPLNTLDGKAYFYQNLKILAFFKTIENLNDTIYHDNPPIFC---RD	355


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; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRN
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11639
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-1

Query Match      78.7%; Score 1934.5; DB 3; Length 464;
Best Local Similarity 79.3%; Pred. No. 4.9e-180; Mismatches 45; Indels 9; Gaps 4;
Matches 365; Conservative 41;

QY 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKSEKKGFRDFILHFLKQRYKII 58
DB 1 MFQPLLDAYVESASTIEKWSKSPPLKIAVANW--GDEEIKFKNVLYFILSQRYTIT 58
QY 59 LHSNPNESDLVFGNPLGQARKILSYQNTKRVYFTGENEVPNFNFDVAIGDFELDFNDR 118
DB 59 LHQNPNESDLVFGNPLGQARKILSYQNTKRVYFTGENEVPNFNFDVAIGDFELDFNDR 118
QY 119 YLRMPLYAYLHYKAMLVNDTTPSYKLK--ALYTKKPSHKFKENHPNLCALIHNESDPW 176
DB 119 YLRMPLYAYLHYKAMLVNDTTPSYKLK--ALYTKKPSHKFKENHPNLCALIHNESDP 176
QY 176 WKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVQNTLGYKVKKNKNEFLSQYKFNLC 235
DB 176 WKRGFASFVASNPNAPIRNAFYDALNSIEPVGGSVQNTLGYKVKKNKNEFLSQYKFNLC 235
QY 236 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDDEALDIYRYL 295
DB 236 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDDEALDIYRYL 295
QY 296 HAQONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKKNLENDTIYHCNDAHYSALHR 355
DB 296 HAQONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKKNLENDTIYHCNDAHYSALHR 355
QY 356 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 401
DB 356 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 401
QY 402 LRNVYDDLRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 456
DB 416 LRNVYDDLRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 470

RESULT 6
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRN
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match      78.5%; Score 1929; DB 2; Length 476;
Best Local Similarity 77.5%; Pred. No. 1.8e-179; Mismatches 39; Indels 24; Gaps 5;
Matches 368; Conservative 39;

QY 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKSEKKGFRDFILHFLKQRYKII 57
DB 1 MFQPLLDADFIESASIEKWSKSPPLKIAVANW--GDEEIKFKNVLYFILSQRYAI 58
QY 58 ILHSNPNESDLVFGNPLGQARKILSYQNTKRVYFTGENEVPNFNFDVAIGDFELDFNDR 117
DB 59 TLHQPNESDLVFGNPLGQARKILSYQNTKRVYFTGENEVPNFNFDVAIGDFELDFNDR 118
QY 118 YLRMPLYAYLHYKAMLVNDTTPSYKLK--ALYTKKPSHKFKENHPNLCALIHNESDP 175
DB 119 YLRMPLYAYLHYKAMLVNDTTPSYKLK--ALYTKKPSHKFKENHPNLCALIHNESDP 178
QY 176 WKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVQNTLGYKVKKNKNEFLSQYKFNLC 235
DB 179 LKRGFASFVASNPNAPIRNAFYDALNSIEPVGGSVQNTLGYKVKKNKNEFLSQYKFNLC 238
QY 236 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDDEALDIYRYL 295
DB 239 FENSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNDDEALDIYRYL 298
QY 296 HAQONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKKNLENDTIYHCNDAHYSALHR 355
DB 299 HTHPNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKKNLENDTIYHCNDAHYSALHR 355
QY 356 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 401
DB 356 DLHEPLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 415
QY 402 LRNVYDDLRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 456
DB 416 LRNVYDDLRDHDLDLRVYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV 470

RESULT 6
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRN
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match      78.5%; Score 1929; DB 2; Length 476;
Best Local Similarity 77.5%; Pred. No. 1.8e-179; Mismatches 39; Indels 24; Gaps 5;
Matches 368; Conservative 39;

QY 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKSEKKGFRDFILHFLKQRYKII 57
DB 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKSEKKGFRDFILHFLKQRYKII 57
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Qy      58  ILHSPNEPSDLVFGNPLEQARKILSYONTKRVYTGGENEVNPNLFDYAI GFDELDFND 117
Db      59  TLHQNPNESSDLVFSNPLGAARKILSYONTKRVYTGGENESPNLFDYAI GFDELDFND 118
Qy     118  RYLRLMPLYAYLHYKAMLVNDTTPSYKLG--ALYTLKKPSHKFKENHPNLCALIHNSDP 175
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Qy     176  WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLC 235
Db     179  LKRGFASVASNANAPRNAPYDALNSIEPTVGGSVRENTLGYKVGKSEFLSQYKFNLC 238
Qy     236  FENSQGYGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFNNDFAIDYIRYL 295
Db     239  FENSQGYGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFNNDFAIDYIKYL 298
Qy     296  HAHQNAVYLDMLYENPLANTIDGKAGFYQDLSPKILDFEKNILENDTIYHCNDAHYSALHR 355
Db     299  HTHPNAVYLDMLYENPLANTIDGKAYFYQDLSPKILDFEKNILENDTIYHNNPFI--YR 355
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Qy     402  LRNVYDDLRDHDLDLRDHERLKSATPLLELSONTSFKIYRKAYOKSLPLRLAI 456
Db     416  LRNVYDDLRVYDDLRVYDRLQNASPLLELSONTSFKIYRKAYOKSLPLRLTI 470

RESULT 7
US-10-189-977A-5
; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane B.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1998-06-05
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-5

Query Match      78.5%; Score 1929; DB 2; Length 476;
Best Local Similarity 77.5%; Pred No. 1.8e-179;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

Qy      1  MFQPLDAFIDSTHLDTHK---PPLNVALANWPLKNSEKKGFRDFILHFIKQRYKI 57
Db      1  MFQPLDAFIESASIEKMWKSPPPPLKIAVANW--GDEEIKFKSVLYFILSQRVAI 58
Qy     58  ILHSPNEPSDLVFGNPLEQARKILSYONTKRVYTGGENEVNPNLFDYAI GFDELDFND 117
Db     59  TLHQNPNESSDLVFSNPLGAARKILSYONTKRVYTGGENESPNLFDYAI GFDELDFND 118
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Db     119  RYLEMPLYAHLHYEAEVLNDTTPYKLGKNSLYALKKPSHHFKENHPNLCVAVNDES 178
Qy     176  WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLC 235
Db     179  LKRGFASVASNANAPRNAPYDALNSIEPTVGGSVRENTLGYKVGKSEFLSQYKFNLC 238
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Qy     176  WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLC 235
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Qy     236  FENSQGYGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFNNDFAIDYIRYL 295
Db     239  FENSQGYGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFNNDFAIDYIKYL 298
Qy     296  HAHQNAVYLDMLYENPLANTIDGKAGFYQDLSPKILDFEKNILENDTIYHCNDAHYSALHR 355
Db     299  HTHPNAVYLDMLYENPLANTIDGKAYFYQDLSPKILDFEKNILENDTIYHNNPFI--YR 355
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Qy     402  LRNVYDDLRDHDLDLRDHERLKSATPLLELSONTSFKIYRKAYOKSLPLRLAI 456
Db     416  LRNVYDDLRVYDDLRVYDRLQNASPLLELSONTSFKIYRKAYOKSLPLRLTI 470

RESULT 8
US-10-392-098A-5
; Sequence 5, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane B.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-5

Query Match      78.5%; Score 1929; DB 3; Length 476;
Best Local Similarity 77.5%; Pred No. 1.8e-179;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

Qy      1  MFQPLDAFIDSTHLDTHK---PPLNVALANWPLKNSEKKGFRDFILHFIKQRYKI 57
Db      1  MFQPLDAFIESASIEKMWKSPPPPLKIAVANW--GDEEIKFKSVLYFILSQRVAI 58
Qy     58  ILHSPNEPSDLVFGNPLEQARKILSYONTKRVYTGGENEVNPNLFDYAI GFDELDFND 117
Db     59  TLHQNPNESSDLVFSNPLGAARKILSYONTKRVYTGGENESPNLFDYAI GFDELDFND 118
Qy     118  RYLRLMPLYAYLHYKAMLVNDTTPSYKLG--ALYTLKKPSHKFKENHPNLCALIHNSDP 175
Db     119  RYLEMPLYAHLHYEAEVLNDTTPYKLGKNSLYALKKPSHHFKENHPNLCVAVNDES 178
Qy     176  WKRGFASVASNPNAPIRNAPYDALNAIEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLC 235
Db     179  LKRGFASVASNANAPRNAPYDALNSIEPTVGGSVRENTLGYKVGKSEFLSQYKFNLC 238
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QY 236 PENSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYL 295
DB 239 PENSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYL 298
QY 296 HAQONAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 355
DB 299 HTHPNAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 355
QY 356 DLNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 401
DB 356 DLNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 415
QY 402 LRVNYDDLRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 456
DB 416 LRVNYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 470

RESULT 9

US-09-092-315-7

; Sequence 7, Application US/09092315

; Patent No. 6399337

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE

; FILE REFERENCE: 07254/049001

; CURRENT APPLICATION NUMBER: US/09/092,315

; CURRENT FILING DATE: 1998-06-05

; EARLIER APPLICATION NUMBER: US 60/048,857

; EARLIER FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-09-092-315-7

Query Match 78.3%; Score 1925.5; DB 2; Length 478;
Best Local Similarity 77.2%; Pred. No. 3.9e-179;
Matches 366; Conservative 41; Mismatches 44; Indels 23; Gaps 5;

QY 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKNSKKGFRDPTILHILKQRYKII 58
DB 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANW--GDEEIKFKNVLYFILLSQRYTIT 58
QY 59 LHSNPNPESDLVFGNPLGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGFDELDFNDR 118
DB 59 LHQNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGFDELDFNDR 118
QY 119 YLRMPLYAYLHYKAMLVNDTTSYKLG--ALYTLKQSPKSHKPNHNPNCALIHNSDPW 176
DB 119 YLRMPLYAYLHYKAMLVNDTTSYKLG--ALYTLKQSPKSHKPNHNPNCALIHNSDPW 176
QY 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSKVNTLGKVKKNKNEFLSOYKENCFC 236
DB 179 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSKVNTLGKVKKNKNEFLSOYKENCFC 238
QY 237 ENSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLH 296
DB 239 ENTQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLH 298
QY 297 AHQONAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 356
DB 299 THKNAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 355
QY 357 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 402
DB 356 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 415
QY 403 RVNYDDLRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 456
DB 416 RINYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 469

RESULT 10

US-09-733-524A-7

; Sequence 7, Application US/09733524A

; Patent No. 6534298

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

; TITLE OF INVENTION: EXPRESSING THEM (amended)

; FILE REFERENCE: 07254-049002

; CURRENT APPLICATION NUMBER: US/09/733,524A

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 09/092,315

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/048,857

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-09-733-524A-7

Query Match 78.0%; Score 1917.5; DB 2; Length 478;
Best Local Similarity 77.0%; Pred. No. 2.3e-178;
Matches 365; Conservative 41; Mismatches 45; Indels 23; Gaps 5;

QY 1 MFQPLLDADFIDSTHLDTHK--PPLNVALANWPLKNSKKGFRDPTILHILKQRYKII 58
DB 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANW--GDEEIKFKNVLYFILLSQRYTIT 58
QY 59 LHSNPNPESDLVFGNPLGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGFDELDFNDR 118
DB 59 LHQNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGENSEPNFNLFDYAIGFDELDFNDR 118
QY 119 YLRMPLYAYLHYKAMLVNDTTSYKLG--ALYTLKQSPKSHKPNHNPNCALIHNSDPW 176
DB 119 YLRMPLYAYLHYKAMLVNDTTSYKLG--ALYTLKQSPKSHKPNHNPNCALIHNSDPW 178
QY 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSKVNTLGKVKKNKNEFLSOYKENCFC 236
DB 179 KRGFASVASNPNAPIRNAFYDALNAIEPVASGSKVNTLGKVKKNKNEFLSOYKENCFC 238
QY 237 ENSQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLH 296
DB 239 ENTQGYGVTEKILDAYFSHTTPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLH 298
QY 297 AHQONAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 356
DB 299 THKNAYLDMLEYENPLNTIDGKAGFYQDLSPEKILDFKNILENDTIYHCNDAHYSALHR 355
QY 357 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 402
DB 356 LNEPLVSV-----DRLRRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 415
QY 403 RVNYDDLRDHDLDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 456
DB 416 RINYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDDLRVYDD 469

RESULT 11

US-10-189-977A-7

; Sequence 7, Application US/10189977A

; Patent No. 6962806

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

;; TITLE OF INVENTION: EXPRESSING THEM (amended)
;; FILE REFERENCE: 07254-049002
;; CURRENT APPLICATION NUMBER: US/10/189,977A
;; CURRENT FILING DATE: 2002-03-07 07:33,524
;; PRIOR APPLICATION NUMBER: US/09/733,524
;; PRIOR FILING DATE: 2000-12-07
;; PRIOR APPLICATION NUMBER: US 09/092,315
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: US 60/048,857
;; PRIOR FILING DATE: 1997-06-06
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 478
;; TYPE: PRF
;; ORGANISM: Helicobacter pylori
US-10-189-977A-7

Query Match 78.0%; Score 1917.5; DB 2; Length 478;
Best Local Similarity 77.0%; Pred. No. 2.3e-178;
Matches 365; Conservative 41; Mismatches 45; Indels 23; Gaps 5;

Qy 1 MFQPLDADFIDSTHLDTHK--PPLNVALANWPLKNSKKGPRDFILHFKQRYKII 58
Db 1 MFQPLDADYVESASIEKXASKSPPLKIAVANW--GDEEIKFKNVLYPILSQRYTIT 58

Qy 59 LHSNPSPDLVFGNPLEQARKILSYONTKRVFTYGENEVNPNLFDYAIGFDELDFNDR 118
Db 59 LHQNPSPDLVFGNPLGSAKILSYQNAKRVFTYGENESPNFNLFDYAIGFDELDFNDR 118

Qy 119 YLRMPLYVAYLHYKAMLVNDTTSYKLLK--ALYTLKPSHKFKENHPNLCAIHNESDPW 176
Db 119 YLRMPLYVAYLHYKAMLVNDTTSYKLLK--ALYTLKPSHKFKENHPNLCAIHNESDPW 176

Qy 177 KRGPASFVSNPNAPIRNAFYDALNAIEPVASGSKVNTLGYKVKKNKNEFLSQYKFNLCF 236
Db 177 KRGPASFVSNPNAPIRNAFYDALNSIEPVVGSGSVNTLGYNVKNKNEFLSQYKFNLCF 238

Qy 237 ENSQGYVTEKILDAYFSHTPIPIYWGSPSVAKDPNPKSFVNVDHFNVDFAIDYIRYLH 296
Db 237 ENSQGYVTEKILDAYFSHTPIPIYWGSPSVAKDPNPKSFVNVDHFNVDFAIDYIRYLH 298

Qy 297 AHQNAVLDMLYENPLNTIDGKAGFYQDLSPEKILDFPKNILENDTIYHCNDAHYSALHRD 356
Db 297 THKNAYLDMLYENPLNTIDGKAGFYQNLSPKILAFPTILENDTIYHDNPFIFC---RD 355

Qy 357 LNEPLVSV-----DDLRRDHDLDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 402
Db 356 LNEPLVTIDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 415

Qy 403 RVNYDDLRRDHDLDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 456
Db 416 RINYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 469

RESULT 12
US-10-392-098A-7
; Sequence 7, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: University of Alberta
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05

;; PRIOR APPLICATION NUMBER: US 09/733,524
;; PRIOR FILING DATE: 2000-12-07
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 478
;; TYPE: PRF
;; ORGANISM: Helicobacter pylori
;; FEATURE:
;; OTHER INFORMATION: H. pylori strain NCTC11639 (763)
;; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-7

Query Match 78.0%; Score 1917.5; DB 3; Length 478;
Best Local Similarity 77.0%; Pred. No. 2.3e-178;
Matches 365; Conservative 41; Mismatches 45; Indels 23; Gaps 5;

Qy 1 MFQPLDADFIDSTHLDTHK--PPLNVALANWPLKNSKKGPRDFILHFKQRYKII 58
Db 1 MFQPLDADYVESASIEKXASKSPPLKIAVANW--GDEEIKFKNVLYPILSQRYTIT 58

Qy 59 LHSNPSPDLVFGNPLEQARKILSYONTKRVFTYGENEVNPNLFDYAIGFDELDFNDR 118
Db 59 LHQNPSPDLVFGNPLGSAKILSYQNAKRVFTYGENESPNFNLFDYAIGFDELDFNDR 118

Qy 119 YLRMPLYVAYLHYKAMLVNDTTSYKLLK--ALYTLKPSHKFKENHPNLCAIHNESDPW 176
Db 119 YLRMPLYVAYLHYKAMLVNDTTSYKLLK--ALYTLKPSHKFKENHPNLCAIHNESDPW 178

Qy 177 KRGPASFVSNPNAPIRNAFYDALNAIEPVASGSKVNTLGYKVKKNKNEFLSQYKFNLCF 236
Db 177 KRGPASFVSNPNAPIRNAFYDALNSIEPVVGSGSVNTLGYNVKNKNEFLSQYKFNLCF 238

Qy 237 ENSQGYVTEKILDAYFSHTPIPIYWGSPSVAKDPNPKSFVNVDHFNVDFAIDYIRYLH 296
Db 237 ENSQGYVTEKILDAYFSHTPIPIYWGSPSVAKDPNPKSFVNVDHFNVDFAIDYIRYLH 298

Qy 297 AHQNAVLDMLYENPLNTIDGKAGFYQDLSPEKILDFPKNILENDTIYHCNDAHYSALHRD 356
Db 297 THKNAYLDMLYENPLNTIDGKAGFYQNLSPKILAFPTILENDTIYHDNPFIFC---RD 355

Qy 357 LNEPLVSV-----DDLRRDHDLDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 402
Db 356 LNEPLVTIDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 415

Qy 403 RVNYDDLRRDHDLDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 456
Db 416 RINYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDL 469

RESULT 13
US-09-092-315-2
; Sequence 2, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRF
; ORGANISM: Helicobacter pylori
US-09-092-315-2

Query Match 77.0%; Score 1892.5; DB 2; Length 486;
Best Local Similarity 75.1%; Pred. No. 6.6e-176;

Db	119	YLRMPLYDRHLHKAESVNDTTSYKLPDLSYALKKPSHHFKENHENLCAVVNNESDPL	178
Qy	177	KRGFASFVASNPNAPINAFYDALNAIEPVASGGSVKNTLGYKVKKNKNEPLSOYKENLCP	236
Db	179	KRGFASFVASNPNAPINAFYDLNSIEPVIGGSVKNTLGYNIKNKSEFLSOYKFNLCF	238
Qy	237	ENSQGYGYVTEKILDAYFSHTIPIYWGSPSAVADFNPKSPVNVHDFNNFDEAIDYIRYLH	296
Db	239	ENSQGYGYVTEKILDAYFSHTIPIYWGSPSAVADFNPKSPVNVCDKDFDEAIDHVRYLH	298
Qy	297	AHQNAYLDMLYENPLNTIDGAGFYQDLSEPKILDPPKNTILENDTIYHCNDAHYSALHRD	356
Db	299	THPNAYLDMLYENPLNTIDGKAYFYQNLSPKILDPFKTILENDTIYHDNPFIF---YRD	355
Qy	357	LNEPLVSV-----DDLRRDHDLLRVNYDDLRVNYDDLRVNYDD	394
Db	356	LNEPLISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD	415
Qy	395	LRVNYDDLRVNYDDLRDHDHLLRRDHERLLSKATPLLELSONTSFKIYRKAYOKSLPLLR	454
Db	416	LRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSONTTFKIYRKAYOKSLPLLR	475
Qy	455	A 455	
Db	476	A 476	

Search completed: August 11, 2006, 19:47:30
Job time : 33.2608 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:46:14 ; Search time 111.112 Seconds
(without alignments)
1901.022 Million cell updates/sec

Title: US-10-764-212-20
Perfect score: 2458
Sequence: 1 MFQPLDAFIDSTHLDTH.....TSFKYKAYOKSLPLRAI 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 209797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 209797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2458	100.0	456	5	US-10-764-212-20
2	1934.5	78.7	464	4	US-10-120-319-1
3	1934.5	78.7	464	4	US-10-189-977-1
4	1934.5	78.7	464	4	US-10-392-098-1
5	1929	78.5	476	3	US-09-733-524-15
6	1929	78.5	476	4	US-10-120-319-5
7	1929	78.5	476	4	US-10-189-977-5
8	1929	78.5	476	4	US-10-392-098-5
9	1925.5	78.3	478	4	US-10-120-319-7
10	1925.5	78.3	478	4	US-10-189-977-7
11	1921.5	78.2	501	3	US-09-733-524-1
12	1917.5	78.0	478	4	US-10-392-098-7
13	1908.5	77.6	436	4	US-10-335-977-8559
14	1897	77.2	479	3	US-09-733-524-17
15	1897	77.2	485	5	US-10-764-212-6
16	1892.5	77.0	486	4	US-10-120-319-2
17	1892.5	77.0	486	4	US-10-189-977-2
18	1892.5	77.0	486	4	US-10-392-098-2
19	1892.5	77.0	486	5	US-10-764-212-2
20	1889	76.9	454	3	US-09-733-524-18
21	1889	76.9	454	4	US-10-120-319-8
22	1889	76.9	454	4	US-10-189-977-8
23	1889	76.9	454	4	US-10-392-098-8
24	1885.5	76.7	485	3	US-09-733-524-2
25	1817	73.9	432	5	US-10-764-212-4
26	1812.5	73.7	446	5	US-10-764-212-16
27	1811.5	73.7	421	4	US-10-335-977-8558

28	1737.5	70.7	440	4	US-10-120-319-3	Sequence 3, Appli
29	1737.5	70.7	440	4	US-10-189-977-3	Sequence 3, Appli
30	1737.5	70.7	440	4	US-10-392-098-3	Sequence 3, Appli
31	1737.5	70.7	440	5	US-10-764-212-18	Sequence 18, Appl
32	1722.5	70.1	440	3	US-09-733-524-3	Sequence 3, Appli
33	1718	69.9	425	4	US-10-120-319-6	Sequence 6, Appli
34	1718	69.9	425	4	US-10-189-977-6	Sequence 6, Appli
35	1718	69.9	425	4	US-10-392-098-6	Sequence 6, Appli
36	1718	69.9	425	5	US-10-764-212-12	Sequence 12, Appl
37	1712.5	69.7	391	5	US-10-764-212-66	Sequence 66, Appl
38	1702.5	69.3	424	3	US-09-733-524-16	Sequence 16, Appl
39	1639	66.7	377	5	US-10-764-212-68	Sequence 68, Appl
40	1558	63.4	372	4	US-10-120-319-13	Sequence 13, Appl
41	1558	63.4	372	4	US-10-189-977-13	Sequence 13, Appl
42	1218	49.6	277	5	US-10-764-212-8	Sequence 8, Appli
43	1129	45.9	227	5	US-10-764-212-25	Sequence 25, Appl
44	1129	45.9	256	5	US-10-764-212-70	Sequence 70, Appl
45	1075.5	43.8	247	5	US-10-764-212-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-10-764-212-20
; Sequence 20, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl P.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 948 FutA fucosyltransferase
US-10-764-212-20

Query Match	100.0%	Score 2458;	DB 5;	Length 456;
Best Local Similarity	100.0%;	Pred. No. 2.2e-195;		
Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFQPLDAFIDSTHLDTHLDETHKPPPLNVALANWWPLKNSKKGFRDFTLHLFKQRYKIILH	60	
Db	1	MFQPLDAFIDSTHLDTHLDETHKPPPLNVALANWWPLKNSKKGFRDFTLHLFKQRYKIILH	60	
QY	61	SNPNPSDLVFNGLPQARKILSYQNTKRVFTGENEVFNFLFDYAIGFDELDFNDRYL	120	
Db	61	SNPNPSDLVFNGLPQARKILSYQNTKRVFTGENEVFNFLFDYAIGFDELDFNDRYL	120	
QY	121	RMPLYAYLHYKAMLVNDTTSYKLLKALYTLKPKSHKFNHNLCAIHNESDPWKRGF	180	
Db	121	RMPLYAYLHYKAMLVNDTTSYKLLKALYTLKPKSHKFNHNLCAIHNESDPWKRGF	180	
QY	181	ASFVASNPNAPIRNAFYDALNAIEPVASGSGVKNTLGYKVKKNKNEFLSQYKFNLCFENSQ	240	
Db	181	ASFVASNPNAPIRNAFYDALNAIEPVASGSGVKNTLGYKVKKNKNEFLSQYKFNLCFENSQ	240	
QY	241	GYGYVTEKILDYFHSHTPIYNGSPSAKDFNPKSPVNVHDFNNDFAIDYIRYLHAQN	300	
Db	241	GYGYVTEKILDYFHSHTPIYNGSPSAKDFNPKSPVNVHDFNNDFAIDYIRYLHAQN	300	
QY	301	AYDMLYENPLNTIDGKAGFYQDLDFEKLIDFVKLENDTIYHCNDAHYSALHRLNEP	360	


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; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-1

Query Match      78.7%; Score 1934.5; DB 4; Length 464;
Best Local Similarity 79.3%; Pred. No. 6.7e-152;
Matches 365; Conservative 41; Mismatches 45; Indels 9; Gaps 4;

Qy 1 MFQPLLDAPIDSTHLDTHK---PPLNVALANWPLKNSEKKGFRDFILHFLKQRYKI 58
Db 1 MFQPLLDAPVESASTEKWSPPLKIAVANW--GDEEIKFKNKSVLYFILSQRYAI 58
Qy 59 LHSNPNEESDLVFGNPLGSAKILSYQNTKRVFYTGGENEVPNPNLFDYAIGDFELDFNDR 118
Db 59 LHSNPNEESDLVFGNPLGSAKILSYQNTKRVFYTGGENEVPNPNLFDYAIGDFELDFNDR 118
Qy 119 YLRMPLYAYLHYKAMLVNDTTPYKLGK--ALYTLKPSHKPKENHPNLCALIHNESDPW 176
Db 119 YLRMPLYAYLHYKAMLVNDTTPYKLGK--ALYTLKPSHKPKENHPNLCALIHNESDPW 176
Qy 177 KRGFASFVASNPNAPIRNAFYDALMAIEPVASGGSVKNTLGYKVNKNKNEFLSQYKFNLCF 236
Db 177 KRGFASFVASNPNAPIRNAFYDALMAIEPVASGGSVKNTLGYKVNKNKNEFLSQYKFNLCF 236
Qy 179 KRGFASFVASNPNAPIRNAFYDALNSIEPVTGGGSRVNTLGYNVKNKNEFLSQYKFNLCF 238
Db 179 KRGFASFVASNPNAPIRNAFYDALNSIEPVTGGGSRVNTLGYNVKNKNEFLSQYKFNLCF 238
Qy 237 ENSQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 296
Db 237 ENSQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 296
Qy 239 ENTQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 298
Db 239 ENTQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 298
Qy 297 AHQNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHRD 356
Db 297 AHQNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHRD 356
Qy 299 THKNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHRD 355
Db 299 THKNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHRD 355
Qy 357 LNEPLVSDLRDRHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 416
Db 357 LNEPLVSDLRDRHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 416
Qy 417 RDHERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 456
Db 416 RVNVERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 455

RESULT 5
US-09-733-524-15
; Sequence 15, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 476
; TYPE: PRT
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; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695A
US-09-733-524-15

Query Match      78.5%; Score 1929; DB 3; Length 476;
Best Local Similarity 77.5%; Pred. No. 2e-151;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

Qy 1 MFQPLLDAPIDSTHLDTHK---PPLNVALANWPLKNSEKKGFRDFILHFLKQRYKI 57
Db 1 MFQPLLDAPIESASTEKWSPPLKIAVANW--GDEEIKFKNKSVLYFILSQRYAI 58
Qy 58 ILHSPNEESDLVFGNPLGSAKILSYQNTKRVFYTGGENEVPNPNLFDYAIGDFELDFNDR 117
Db 59 TLHQPNNEESDLVFNPLGAARKILSYQNTKRVFYTGGENEVPNPNLFDYAIGDFELDFNDR 118
Qy 118 YLRMPLYAYLHYKAMLVNDTTPYKLGK--ALYTLKPSHKPKENHPNLCALIHNESDP 175
Db 119 YLRMPLYAYLHYKAMLVNDTTPYKLGK--ALYTLKPSHKPKENHPNLCALIHNESDP 178
Qy 176 WKRGFASFVASNPNAPIRNAFYDALMAIEPVASGGSVKNTLGYKVNKNKNEFLSQYKFNLC 235
Db 179 LKRGFASFVASNPNAPIRNAFYDALNSIEPVTGGGSRVNTLGYKVNKNKNEFLSQYKFNLC 238
Qy 236 FENSQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 295
Db 239 FENSQGYGVTEKILDAYFESHPIYWGSPSVAKDNPKSFVNVHDPNPNDEAIDYIRYL 298
Qy 296 HAQNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHR 355
Db 299 HTHPNAYLDMLENPLNTIDGKAGFYQDLSFEKILDFKKNILENDTIYHCNDHAHYSALHR 355
Qy 356 DLNEPLVSV-----DRLRDRHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 401
Db 356 DLNEPLVSDLRDRHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 415
Qy 402 LRVNYDDLRDRHDDLRDRHERLLSKATPILLESQNTSFKIYKAYOKSLPLLRAI 456
Db 416 LRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 470

RESULT 6
US-10-120-319-5
; Sequence 5, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-5

Query Match      78.5%; Score 1929; DB 4; Length 476;
Best Local Similarity 77.5%; Pred. No. 2e-151;
Matches 368; Conservative 39; Mismatches 44; Indels 24; Gaps 5;

Qy 1 MFQPLLDAPIDSTHLDTHK---PPLNVALANWPLKNSEKKGFRDFILHFLKQRYKI 57
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[illegible]

RESULT 9

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US-10-120-319-7
; Sequence 7, Application US/10120319
; Publication No. US2002016479A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRt
; ORGANISM: Helicobacter pylori
US-10-120-319-7

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RESULT 10

RESULT 10
 US-10-189-977-7
 ; Sequence 7, Application US/10189977
 ; Publication NO. US20030166211A1
 ; PRIOR APPLICATION NUMBER: 60/048,857
 ; CORRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 09/092,315
 ; PRIOR FILING DATE: 1998-06-05

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; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
US-09-733-524-1

Query Match
Best Local Similarity 78.2%; Score 1921.5; DB 3; Length 501;
Matches 364; Conservative 41; Mismatches 46; Indels 9; Gaps 4;

Qy 1 MFQPLDAFIDSTHLDTHK--PPLNVALANWPLKNSEKKGFRDFTLHFLKQRYKII 58
Db 1 MFQPLDAYVESASIERWASKSPPLKIAVANW--GDDEIKFKNVLYFILSQRYTIT 58
Qy 59 LHSNPBPSDLVFCNPLEQARKILSYQNTKRVFTYTGNEVFNFLFDYAIGFDELDFNDR 118
Db 59 LHSNPBPSDLVFCNPLGSAKILSYQNAKRVFTYTGNESEFNFLFDYAIGFDELDFNDR 118
Qy 119 YLRMPLYAYLHYKAMLVNDTTSYK--ALYTLKPSHKFKNHNPNCALIHNSDPW 176
Db 119 YLRMPLYAYLHYKAMLVNDTTSYK--ALYTLKPSHKFKNHNPNCALIHNSDPW 176
Qy 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGGSVNTLGYKVKKNKNEFLSQYKPNLCF 236
Db 177 KRGFASVASNPNAPIRNAFYDALNSIEPTVGGSVRNTLGYNVKNKNEFLSQYKPNLCF 238
Qy 237 ENSQGYGVTEKILDAFVSHTIPIYWGSPSVAKDPNPKSFVNVHDFNNDFDAIDYIRYLH 296
Db 237 ENSQGYGVTEKILDAFVSHTIPIYWGSPSVAKDPNPKSFVNVHDFNNDFDAIDYIRYLH 296
Qy 299 THKNAYLDMLYENPLNTIDGKAGFYQDLSFKILDFKNIILENTIYHCNDAHYSALHRD 356
Db 299 THKNAYLDMLYENPLNTIDGKAGFYQDLSFKILDFKNIILENTIYHCNDAHYSALHRD 356
Qy 357 LNEPLVSV-----DRLRDHDLRVNVDLRYNDDLRVNYDDLRVNYDDLRVNYDDL 416
Db 357 LNEPLVSV-----DRLRDHDLRVNVDLRYNDDLRVNYDDLRVNYDDLRVNYDDL 416
Qy 417 RDRHERLLSKATPILLESQNTSKYKAYOKSLPLLRAI 456
Db 416 RVNYERLLSKATPILLESQNTSKYKAYOKSLPLLRAI 455

RESULT 12
US-10-392-098-7
; Sequence 7, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-7
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Query Match
Best Local Similarity 78.0%; Score 1917.5; DB 4; Length 478;
Matches 365; Conservative 41; Mismatches 45; Indels 23; Gaps 5;

Qy 1 MFQPLDAFIDSTHLDTHK--PPLNVALANWPLKNSEKKGFRDFTLHFLKQRYKII 58
Db 1 MFQPLDAYVESASIERWASKSPPLKIAVANW--GDDEIKFKNVLYFILSQRYTIT 58
Qy 59 LHSNPBPSDLVFCNPLEQARKILSYQNTKRVFTYTGNEVFNFLFDYAIGFDELDFNDR 118
Db 59 LHSNPBPSDLVFCNPLGSAKILSYQNAKRVFTYTGNESEFNFLFDYAIGFDELDFNDR 118
Qy 119 YLRMPLYAYLHYKAMLVNDTTSYK--ALYTLKPSHKFKNHNPNCALIHNSDPW 176
Db 119 YLRMPLYAYLHYKAMLVNDTTSYK--ALYTLKPSHKFKNHNPNCALIHNSDPW 176
Qy 177 KRGFASVASNPNAPIRNAFYDALNAIEPVASGGSVNTLGYKVKKNKNEFLSQYKPNLCF 236
Db 177 KRGFASVASNPNAPIRNAFYDALNSIEPTVGGSVRNTLGYNVKNKNEFLSQYKPNLCF 238
Qy 237 ENSQGYGVTEKILDAFVSHTIPIYWGSPSVAKDPNPKSFVNVHDFNNDFDAIDYIRYLH 296
Db 237 ENSQGYGVTEKILDAFVSHTIPIYWGSPSVAKDPNPKSFVNVHDFNNDFDAIDYIRYLH 296
Qy 299 THKNAYLDMLYENPLNTIDGKAGFYQDLSFKILDFKNIILENTIYHCNDAHYSALHRD 356
Db 299 THKNAYLDMLYENPLNTIDGKAGFYQDLSFKILDFKNIILENTIYHCNDAHYSALHRD 356
Qy 357 LNEPLVSV-----DRLRDHDLRVNVDLRYNDDLRVNYDDLRVNYDDLRVNYDDL 402
Db 357 LNEPLVSV-----DRLRDHDLRVNVDLRYNDDLRVNYDDLRVNYDDLRVNYDDL 415
Qy 403 RVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDL 456
Db 416 RINYDDLRVNYDDLRVNYERLLSKATPILLESQNTSKYKAYOKSLPLLRAI 469

RESULT 13
US-10-335-977-8559
; Sequence 8559, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8559:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...436
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8559:
US-10-335-977-8559

Query Match          77.6%; Score 1908.5; DB 4; Length 436;
Best Local Similarity 79.3%; Pred. No. 8.9e-150;
Matches 363; Conservative 26; Mismatches 36; Indels 33; Gaps 4;

QY 1 MFQPLDADFIDSTHLDLDE--TTHKPPPLNVALANWMLKNSKKGFRDFILHFKLQRYKIIILH 60
DB 1 MFQPLDADTSDTRLDLDETDYKPLNIALANWPLDKRESKGRFRFILYFILSQRVITILH 60

QY 61 SNPNPESDLVFGNPLEQARKILSYQNTKRVFTGTGENEVPNFMFLDYAIGFDELDNDRYL 120
DB 61 QNPNEPSDLVFGSPIGSARKILSYQNTKRVFTGTGENEVPNFMFLDYAIGFDELDNDRYL 120

QY 121 RPLVYAVLYHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLICALIHNESDPWKR 178
DB 121 RPLVYAVLYHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLICALIHNESDPWKR 178

QY 179 GFASVFNAPNAPIRNAFYDALNAIEPVASGSGVNTLGYKVNKNKNEFLSQYKFNLC 238
DB 179 RPLVYAVLYHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLICALIHNESDPWKR 180

QY 181 GFASVFNAPNAPIRNAFYDALNIEPTVGGSGVNTLGYKVNKNKNEFLSQYKFNLC 240
DB 181 GFASVFNAPNAPIRNAFYDALNIEPTVGGSGVNTLGYKVNKNKNEFLSQYKFNLC 240

QY 239 SQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPKSFVNVDHFNFDNDEAIDYIRYLHAH 298
DB 241 TQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPKSFVNVDHFNFDNDEAIDYIRYLHAH 300

QY 299 QNAYLDMLYENPLNTIDGKAGFYQDLSPEKILDPFNKILNDNTIYHCNDHAYSAHLRDLN 358
DB 301 PNAYLDMLYENPLNTIDGKAGFYQDLSPEKILDPFNKILNDNTIYHCNDHAYSAHLRDLN 357

QY 359 EPLVSVDDLRRDHDLDRLVNYDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 418
DB 358 EPLVSVDDLRRDHDLDRLVNYDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 427

QY 419 DHERLLSKATPLLELSQNTSFKIYKAYQKSLPLLRAL 456
DB 393 ---RLQNASPLLELSQNTSFKIYKAYQKSLPLLRAL 427

RESULT 14
US-09-733-524-17
; Sequence 17, Application US/09733524
; Patent No. US20020068347A1
;
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 479

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; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PRTIDE
; LOCATION: (0) ... (0)
; OTHER INFORMATION: Strain 763 from NCTC11639
US-09-733-524-17

Query Match          77.2%; Score 1897; DB 3; Length 479;
Best Local Similarity 76.4%; Pred. No. 9.2e-149;
Matches 363; Conservative 42; Mismatches 46; Indels 24; Gaps 6;

QY 1 MFQPLDADFIDSTHLDLDE--TTHKPPPLNVALANWMLKNSKKGFRDFILHFKLQRYKIIILH 58
DB 1 MFQPLDADTSDTRLDLDETDYKPLNIALANWPLDKRESKGRFRFILYFILSQRVITILH 58

QY 59 LHSNPNPESDLVFGNPLEQARKILSYQNTKRVFTGTGENEVPNFMFLDYAIGFDELDND 117
DB 59 LHSNPNPESDLVFGNPLEQARKILSYQNTKRVFTGTGENEVPNFMFLDYAIGFDELDND 118

QY 118 RYLRLMPLVYAVLYHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLICALIHNESDP 175
DB 119 RYLRLMPLVYAVLYHYKAMLVNDTTPSYKLGK--ALYTLKPKSHKPKENHPNLICALIHNESDP 178

QY 176 WTRGFASVFNAPNAPIRNAFYDALNAIEPVASGSGVNTLGYKVNKNKNEFLSQYKFNLC 235
DB 179 LKRGFASVFNAPNAPIRNAFYDALNIEPTVGGSGVNTLGYKVNKNKNEFLSQYKFNLC 238

QY 236 FNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPKSFVNVDHFNFDNDEAIDYIRYL 295
DB 239 FNTQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPKSFVNVDHFNFDNDEAIDYIRYL 298

QY 296 HAHQNAVLDMLYENPLNTIDGKAGFYQDLSPEKILDPFNKILNDNTIYHCNDHAYSAHLR 355
DB 299 HTHKNAYLDMLYENPLNTIDGKAGFYQDLSPEKILDPFNKILNDNTIYHCNDHAYSAHLR 355

QY 356 DLNEPLVSV-----DRLRRDHDLDRLVNYDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 401
DB 356 DLNEPLVSV-----DRLRRDHDLDRLVNYDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDD 415

QY 402 LRNVYDDLRRDHDLDRLVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 456
DB 416 LRNVYDDLRRDHDLDRLVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 470

RESULT 15
US-10-764-212-6
; Sequence 6, Application US/10764212
; Publication No. US20050164338A1
;
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1218 FutB fucosyltransferase
US-10-764-212-6

Query Match          77.2%; Score 1897; DB 5; Length 485;
Best Local Similarity 75.4%; Pred. No. 9.3e-149;
Matches 362; Conservative 41; Mismatches 47; Indels 30; Gaps 5;

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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:47:49 ; Search time 17.3294 Seconds
(without alignments)
1771.230 Million cell updates/sec

Title: US-10-764-212-20
Perfect score: 2458
Sequence: 1 MFQPLDAPIDSTHLEDTTH.....TSFKYKAYQKSLPLRAI 456

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Cellerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	6.1	406	7	US-11-197-712-284
2	147.5	6.0	302	6	US-10-953-349-5129
3	147.5	6.0	323	6	US-10-953-349-5128
4	147.5	6.0	338	6	US-10-953-349-5127
5	138	5.6	513	6	US-10-449-902-52598
6	131	5.3	336	7	US-11-293-697-4748
7	129.5	5.3	246	6	US-10-449-902-44967
8	123.5	5.0	1781	6	US-10-537-642-24
9	119.5	4.9	3029	6	US-10-537-642-10
10	116.5	4.7	2024	6	US-10-537-642-21
11	116.5	4.7	2133	6	US-10-537-642-9
12	111.5	4.5	1464	6	US-10-537-642-27
13	111.5	4.5	2397	6	US-10-471-571A-2632
14	111	4.5	554	6	US-10-471-571A-5504
15	110.5	4.5	1050	6	US-10-471-571A-4624
16	108	4.4	126	6	US-10-126-915-4
17	102.5	4.2	414	6	US-10-471-571A-5608
18	102.5	4.2	1815	6	US-10-537-642-19
19	102	4.1	895	6	US-10-471-571A-922
20	101.5	4.1	1125	7	US-10-294-155-12
21	97.5	4.0	787	6	US-10-392-874A-2
22	97.5	4.0	807	6	US-10-449-902-43388
23	97.5	4.0	2404	6	US-10-537-642-3
24	97	3.9	178	6	US-10-953-349-34473
25	97	3.9	178	7	US-11-056-355B-11955

ALIGNMENTS

RESULT 1

US-11-197-712-284

; Sequence 284, Application US/11197712

; Publication No. US20060130160A1

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bouqueleret, Lydie

; APPLICANT: Jobert, Severin

; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

; FILE REFERENCE: 78.US4.CIP

; CURRENT FILING DATE: 2005-08-04

; PRIOR APPLICATION NUMBER: US/11/197,712

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US/09/876,997

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/187,470

; PRIOR FILING DATE: 2000-03-06

; PRIOR APPLICATION NUMBER: US 60/169,629

; PRIOR FILING DATE: 1999-12-08

; NUMBER OF SEQ ID NOS: 482

; SOFTWARE: Patent.pm

; SEQ ID NO 284

; LENGTH: 406

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -31...-1

US-11-197-712-284

Query Match 6.1%; Score 149; DB 7; Length 406;

Best Local Similarity 27.6%; Pred. No. 0.00011;

Matches 66; Conservative 37; Mismatches 82; Indels 54; Gaps 12;

QY 83 SYONTKRYFTGENEVPNPNFDYAGPDELDPNDRLRMPLYAYLVHYKAMLVNDTSP 142

DB 193 SPKNYKLFHK-----PVITLFNYTATF-----SRHSHLPLTTQYLE-----SI 231

QY 143 YKIKALYTLKKPSHKFNHPNLCALIHNES--DPMKRGFASVFASNPAPINAFVDA 200

DB 232 EVLKSRLYL-VPLQSKNKLKRLAFLVYVQSCDP-----PSDRSYVR-----ELM 277

QY 201 NAEIPVAGSGSVKN-TLGYKVKNK-----NEFLSQYKFNLCFNSQGYGVYTKILD 251

DB 278 TVIEVDSYGECLRNKDLFQQLKNPASMADGFPRIIAQYKFIAPENAVCDYITEKFWR 337

QY 252 AYFSHTIPIYWGSPSVAQDFNP--KSFVNVDHFNDFDAIDYIRYLHAKQNALDMLYE 308

Sequence 34472, A
Sequence 11954, A
Sequence 23, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 15, Appli
Sequence 80733, A
Sequence 80731, A
Sequence 3528, Ap
Sequence 3, Appli
Sequence 98565, A
Sequence 109804,
Sequence 98564, A
Sequence 109803,
Sequence 98563, A
Sequence 109802,
Sequence 18453, A
Sequence 6, Appli
Sequence 5, Appli

US-10-953-349-34472
US-11-056-355B-11954
US-10-537-642-23
US-10-530-234-8
US-11-257-500-9
US-11-257-500-15
US-11-056-355B-80733
US-11-056-355B-80732
US-11-056-355B-80731
US-10-471-571A-3528
US-10-126-915-3
US-11-056-355B-98565
US-11-056-355B-109804
US-11-056-355B-98564
US-11-056-355B-109803
US-11-056-355B-98563
US-11-056-355B-109802
US-11-330-403-18453
US-10-537-642-6
US-10-537-642-5

26 97 3.9 261 6
27 97 3.9 261 7
28 97 3.9 2647 6
29 96 3.9 789 6
30 95.5 3.9 1517 7
31 95.5 3.9 1526 7
32 95 3.9 1990 7
33 95 3.9 2031 7
34 95 3.9 2041 7
35 94.5 3.8 953 6
36 94 3.8 56 6
37 94 3.8 2041 7
38 94 3.8 2041 7
39 94 3.8 2054 7
40 94 3.8 2054 7
41 94 3.8 2073 7
42 94 3.8 2073 7
43 93.5 3.8 430 7
44 93.5 3.8 1062 6
45 93 3.8 400 6


```
Db 282 ENSNEEDVTEKFQSLVGTGAIPIVIGAPNI-QEFSPEGAILHIKELDDVPSIAKTMKH 340
Qy 295 LHAHQAYLMDL--YENPLNTIDGKAGFYQDLSFEKILD 331
Db 341 IASNQAFNQLRWKIDGSPD-----SPKALID 368

RESULT 6
US-11-293-697-4748
; Sequence 4748, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4748
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4748

Query Match 5.3%; Score 131; DB 7; Length 336;
Best Local Similarity 24.1%; Pred. No. 0.0028;
Matches 58; Conservative 41; Mismatches 72; Indels 70; Gaps 14;

Qy 115 FNDYRLMPLYAYLHYKAMLVNDTT-----SPYKLK---ALYTLKKPSH----KFKENHP 163
Db 71 FN-KPIALPRCSIEVHREVMYNPISQALPRSPRRGQRWIFWFSMESPSHCWOLKAWDGYF 129
Qy 164 NLCALIHNESD-----PW-----KRGFASFVASN--PNAPIRANFYDA 199
Db 130 NLTWYSRSDSIFTPYGWLEFWGQAPHPPLNLSAKTELVAWAVSNWGPNS-ARVRYTQS 188
Qy 200 LNA-----IEPVASGGSVKNTLGYKVKKNNEFLSQYKFNLCFNSQGYGVVTEKI 249
Db 189 LQAHKVDVYGRSHKPLPQGTMM-----ETLSRYKFVLAFLNSLHPDVIITEKL 236
Qy 250 ----LDAYFSHTIPIYWGSPS---VAKDFNPKSFVNVHDFNFDFAIDYIRYLHAHQAY 302
Db 237 WRNLEAW---AVPVVLG-PSRSNYERFLPPDAFIHVDDFQSPKDLARYLQELDKDHARY 292

Qy 303 L 303
Db 293 L 293

RESULT 7
US-10-449-902-44967
; Sequence 44967, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44967
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```
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44967

Query Match 5.3%; Score 129.5; DB 6; Length 246;
Best Local Similarity 22.9%; Pred. No. 0.0024;
Matches 55; Conservative 45; Mismatches 89; Indels 51; Gaps 10;

Qy 109 GFDELDNDYRLMPLYAYLHYKAMLVNDTTSPYKLYKALYTLKKPSHKFKENHPNLCAL 168
Db 20 GFEDI-----FIGTHAK--DDVQVTYAKSFHT--SRSHVHSTERND--AL 60
Qy 169 IHNES-----DPWKRGFASFVASNPNAPIRANFYDALNAIBPVASGGSVKNTLGYKVK 221
Db 61 IYWSSSRCLPHEDKVAQDFLSLP-----HHSFGKLANVD-----GPDMLSM-YPVC 108
Qy 222 NQNE-----FLSQYKFNLCFNSQGYGVVTEKILDYFHSHTIPIYWGSPSVAK 269
Db 109 STNDNGKPHWDHLHCAMSHYKFLVAIENTKTESYVTEKLFYALEAGSVPIYFGAPNVMD 168
Qy 270 DENPKSFVNVHDPNPFDEAIDYIRYLHAHQAYLMDLYENPLNTIDGKAGFYQDLSFEKI 329
Db 169 FIPNSIIDASKFSLRELASVYKAVANDPVAYAYAHWRRCGTL--GNFGRSREMSLDTL 227

RESULT 8
US-10-537-642-24
; Sequence 24, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 1781
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-24

Query Match 5.0%; Score 123.5; DB 6; Length 1781;
Best Local Similarity 19.0%; Pred. No. 0.13;
Matches 79; Conservative 75; Mismatches 159; Indels 103; Gaps 19;

Qy 72 GNPLEQARKILSYQNTKRVFYTGGENEVPNLFYDAIGAIFDELDFNDYRLMPLYAYLHY 131
Db 648 GDHIKSGDTIKNVENF--VNTNSNNISNINI-----SINCNN-----YEKVINN 690
Qy 132 KAMLVNDTTSPYKLYKALYTLKKPSHKFKENHPN-----LCALIHNESDPWKGPASFVA 185
Db 691 MSFINNKESNINKDDVYNGNMNDNHNHVNNTLNTSLSDLCNSNSESSEKKQEAIVCLN 750
Qy 186 SNPNAPI-----RNAFYDALNAIBPVASGGSVKNTLGYKVKKNNEFLSQYKFNLCF 236
Db 751 KNDTHDIIKNTVSNKKRFSLY-----MNPINNNTNNNNNDTSTNVQFINNY----- 799
Qy 237 ENSQGYGVVTEKILDYFHSHTIPIYWGSPSVAKDFNPKSFVNV-----HDF 282
Db 800 --TNDYFYDEKDEE--QH-----NPDYKNNKKNKGRNINIRIKKEDSQEHTNEK 848
```



```

US-10-537-642-9
; Sequence 9, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 2133
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-9

Query Match 4.7%; Score 116.5; DB 6; Length 2133;
Best Local Similarity 19.4%; Pred. No. 0.64;
Matches 93; Conservative 89; Mismatches 175; Indels 123; Gaps 23;

QY 26 VALANWPLKNSK--KGPRDFILHLPILKORYKIIILHSNPNESDLVFGNPLBQARKILS 83
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1159 IILLNKWAKPGIENCIELFYSHLHYVIK-KYIIDIINKSKCKEIKLYLPQLVQSLRTFN 1217

QY 84 YQNTKRVFTG--ENEVPNENLDYAIGPDELDEFNDEYLEMPLYAYLHYKMLVND--T 139
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1218 YOHIDNLFIINTLIQKCIKSKGSIYFYWFLLSAKOK-IRGKL---YLHTHKLFINKLMT 1273

QY 140 TSPYKALKALYTLKPKSHKFNENPNICALIHNSSDPMK-----RGFASPVASN----- 187
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1274 SNIRKNIILDLKQNRFRNQLLYLTAKAKTDRIONKTRKLRNPLFYRTNYGYINI 1333

QY 188 NPAITRNAF-----YDAL-----NAIEPVASGVS-----KN 214
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1334 KDFIKNIIFSDHNVDLFDICKRKRENSLDTPMRGDNIQPSYLGMPGKSTDDSKN 1393

QY 215 TLG-----YKVKQKHEFLSOYKFNICFENSQGYGYTEKILDAYSHHTIPIYW-GSPSV 267
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1394 VYGDGNKNYVGDGNKYVGDGSKNIYCDNKNYVGDGNKNI---YGDGSKNIYGDGNKNI 1450

QY 268 AKDENPKSFVNVHDFNDFEADIVRYLHAHQAYLDMLYENPLNTIDGKAGFYQDLSPF 327
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1451 FSDDNK---NLVSDNNNNKHRYNKIV-----KNISYE 1480

QY 328 KILDPFKNILENTIYHCNDHAHYSALHRLNBEFLVSVDLLRRDHDHLRVNY-----DDL--- 381
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1481 HFNEYYPDNKSRNIYTCN-----KOICSIYYLD-----NELTINYDIKODLYFF 1526

QY 382 --RVNYDRLRVNYDRLRVNYDRLRVNYDRLRRDHDHLRRDHEHLLSKATPLLELSQNTSF 439
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 1527 QYKRSSDEKLLN--TDLSDNSNDM--IHVID---DSKNVKIERNRDNPSFFSNFLQFNLDLF 1581

RESULT 12
US-10-537-642-27
; Sequence 27, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.

```



```

Qy 64 -----NEPSDLVFGN--PLEQARKILSYQNTKRVFTYTGNE-----VPNFN 102
Db 175 LKKWDKAYDEYFVLSNKKOGLFGHYVAIEYVKDSLDLPQPEFNSPFI SDIEKARKSPNOT 234
Qy 103 LFDYAIGPD-----ELDPN-----RMP-----LYYAVLHYKAMLVNDTTSPY 143
Db 235 LIDYIEGVVEESQRIEVDENKEMFDFKFLHPSRLPDGRWPSQTEFRLSLMOQLAVNQITSGN 294
Qy 144 K-----LKALY---TLKKPSHKPKENHPN---LCALIHNESDPW-----K 177
Db 295 ERISVNGPPTGKTTLLKOIFAHLVVERGKELAKLNNPKDAFVTKIHETDDKYVYLLK 354
Qy 178 RGFASF---VASNENAPIRNAPYDALNAIEPVASGGSVKN-----TLGYKV 220
Db 355 ESIKYKMWVASSNNGAVENISKD-LPKIEEI-----IRNPEKCKPKYEQNYANLAHEL 408
Qy 221 XNKNFELSQYKFNLCPFENSQG-----YQVTEKILDAYFSHTIPTIYWGSPSVAKDFNPKS 275
Db 409 KDFAEIAE---DLIGESAWGLFSGVFGKSTN--INQVLSHML-----KQDANDIG 453
Qy 276 FVNVDHFNWPEADYIYRL---HAHQNAYL-----DMLYENPLNTIDGKAGFYQDLSF 326
Db 454 FAKL--LQNNENRMSYNELMSEWQSHORAFLEELRHVEMLKKEESIRAYDVYVKNCESFSKI 511
Qy 327 EKILDFPKNILENDTIYHCNDAHYSALHRDLNEPLVSVDDLRRDHDLDLRVNYDDLVRVND 386
Db 512 EQVINSEKTSIE-EQVYHLD-----NETL-----RDNKEI-----E 541
Qy 387 DLRVNYDDLVRVNYDDLVRVNYDDLRRDHDLDLRVNYDDLRRDHDLDLRVNYDDLRRDHDLDLRVNYDDL 446
Db 542 DL-----DNRINY--IVKQIETLNELIKSIKESNKGFINKLKAMFNSBEDESYPKHNEK 594
Qy 447 QKSL 450
Db 595 QQLL 598

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Search completed: August 11, 2006, 19:54:01
Job time : 19.3294 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2006, 19:53:30 ; Search time 118.313 Seconds
(without alignments)
1723.552 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 446

Sequence: 1 MFQPLLDAYVESIERKAS.....KIYKAYQKPIKNPPYCAP 446

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446	100.0	446	9	Aeb70145 Helicobac
2	68	15.2	247	9	Aeb70205 H. pylori
3	68	15.2	256	9	Aeb70199 H. pylori
4	68	15.2	277	8	Adj77816 Helicobac
5	68	15.2	277	8	Adj27351 Alpha-1,3
6	68	15.2	277	9	Aeb70137 Helicobac
7	59	13.2	486	8	Adj77810 Helicobac
8	59	13.2	486	8	Adj27345 Alpha-1,3
9	59	13.2	486	9	Aeb70131 Helicobac
10	54	12.1	245	9	Aeb70201 H. pylori
11	54	12.1	391	9	Aeb70195 H. pylori
12	54	12.1	432	8	Adj77812 Helicobac
13	54	12.1	432	8	Adj27347 Alpha-1,3
14	54	12.1	432	9	Aeb70141 Helicobac
15	53	11.9	418	5	Abu52257 Helicobac
16	53	11.9	424	5	Abg30885 H. pylori
17	53	11.9	425	8	Adj77820 Helicobac
18	53	11.9	425	8	Adj27355 Alpha-1,3
19	53	11.9	425	9	Aeb70141 Helicobac
20	53	11.9	476	5	Abg30884 H. pylori
21	50	11.2	456	9	Aeb70149 Helicobac
22	48	10.8	231	9	Aeb70193 H. pylori
23	48	10.8	246	9	Aeb70204 H. pylori

ALIGNMENTS

RESULT 1

AEB70145
ID AEB70145 standard; protein; 446 AA.

XX AC AEB70145;

DT 06-OCT-2005 (first entry)

DE Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 16.

KW Fucosyltransferase; protein production; enzyme.

XX OS Helicobacter pylori; strain 1111.

XX FH Key Location/Qualifiers
FT Misc-difference 168 /note= "Encoded by GC"
FT Misc-difference 355 /note= "Encoded by AG"
FT Misc-difference 408 /note= "Encoded by AG"
FT Misc-difference 435 /note= "Encoded by AG"

XX US2005164338-A1.

XX 28-JUL-2005.

XX 22-JAN-2004; 2004US-00764212.

XX 22-JAN-2004; 2004US-00764212.

XX (NEOS-) NEOSE TECHNOLOGIES INC.

XX (UYAL-) UNIV ALBERTA.

XX Simala-Grant J, Taylor D, Johnson KP, Bezila DJ;

XX WPI; 2005-521417/53.

XX N-PSDB; AEB70144.

XX New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

XX Claim 1; SEQ ID NO 16; 97pp; English.

XX The present invention provides alpha-1,3/4-fucosyltransferase (also

CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.
XX
SQ Sequence 446 AA;

Query Match 100.0%; Score 446; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLDAYVESASIEKQASKSPPLKIAVANWGWDEIKFKKSVLYFIPSQRYTIALH 60
Db 1 MFQPLDAYVESASIEKQASKSPPLKIAVANWGWDEIKFKKSVLYFIPSQRYTIALH 60

Qy 61 QNPNEFSDLVFSPNPLGSAKILSYQNAKRVFYTTGENEVPNPNLFDYAIGFDELDFDRYL 120
Db 61 QNPNEFSDLVFSPNPLGSAKILSYQNAKRVFYTTGENEVPNPNLFDYAIGFDELDFDRYL 120

Qy 121 RMPLYYDRLHKAESVNDTTSPPYKLDNSLYTLKPKSHQFKENHPNLCVVNDSDPLKR 180
Db 121 RMPLYYDRLHKAESVNDTTSPPYKLDNSLYTLKPKSHQFKENHPNLCVVNDSDPLKR 180

Qy 181 GVVSFVASNANAPMRNAPYDALNSIEPVTGGGSKNTLGYNNKNSRFLSOYKNCNCFEN 240
Db 181 GVVSFVASNANAPMRNAPYDALNSIEPVTGGGSKNTLGYNNKNSRFLSOYKNCNCFEN 240

Qy 241 SQGYYVTEKILDYFHSHTIPIYWGSPVAKDFNPFVNVHDFNPFDEADYIKYLHTH 300
Db 241 SQGYYVTEKILDYFHSHTIPIYWGSPVAKDFNPFVNVHDFNPFDEADYIKYLHTH 300

Qy 301 PNAYLDMLYENPLNALDGKAYFYQDLSPFKILAFKTLILENDTIYHKSSTSFMECDLDE 360
Db 301 PNAYLDMLYENPLNALDGKAYFYQDLSPFKILAFKTLILENDTIYHKSSTSFMECDLDE 360

Qy 361 PLASIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL 420
Db 361 PLASIDDLRVNDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL 420

Qy 421 SONTSPKIYKAYOKPIKNPYPCAP 446
Db 421 SONTSPKIYKAYOKPIKNPYPCAP 446

RESULT 2
AEB70205
ID AEB70205 standard; protein; 247 AA.
XX
AC AEB70205;
XX
DT 06-OCT-2005 (first entry)
XX
DE H. pylori fucosyl transferase, FutB, protein, ORF19C2B.pep SEQ ID NO: 76.
XX
KW Fucosyltransferase; protein production.
XX
OS Helicobacter pylori; strain 19C2.
XX
FN US2005164338-A1.
XX
PD 28-JUL-2005.
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX

DR WPI; 2005-521417/53.
XX
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Disclosure; SEQ ID NO 76; 97pp; English.
XX

CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase (amino acids 1-247)
CC protein fragment.
XX

SQ Sequence 247 AA;

Query Match 15.2%; Score 68; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSAKILSYQNAKRVFYTTGENEVPNPNLFDYAIGFDELDFDRYLRLHKK 132
Db 74 NPLGSAKILSYQNAKRVFYTTGENEVPNPNLFDYAIGFDELDFDRYLRLHKK 133

Qy 133 AESVNDTT 140
Db 134 AESVNDTT 141

RESULT 3
AEB70199
ID AEB70199 standard; protein; 256 AA.
XX
AC AEB70199;
XX
DT 06-OCT-2005 (first entry)
XX
DE H. pylori fucosyl transferase, FutB, protein fragment, SEQ ID NO: 70.
XX
KW Fucosyltransferase; protein production; enzyme.
XX
OS Helicobacter pylori; strain 19C2.
XX
FN US2005164338-A1.
XX
PD 28-JUL-2005.
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX

DR WPI; 2005-521417/53.
XX
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Disclosure; SEQ ID NO 70; 97pp; English.
XX

CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase catalytic domain
CC (amino acids 22-277) protein fragment.
XX

XX SQ Sequence 256 AA;
Query Match 15.2%; Score 68; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 132
|||||
DB 74 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 133
|||||

QY 133 AESVNDTT 140
|||||
DB 134 AESVNDTT 141
|||||

RESULT 4
ADJ77816
ID ADJ77816 standard; protein; 277 AA.
XX
AC ADJ77816;
XX
DT 06-MAY-2004 (first entry)
XX
DE Helicobacter pylori strain 19C2 FutB protein SeqID 8.
XX
KW FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX
OS Helicobacter pylori.
XX
PN WO2004009838-A2.
XX
PD 29-JAN-2004.
XX
PF 23-JUL-2003; 2003WO-US023057.
XX
PR 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Johnson KF, Bezila DJ;
XX
DR WPI; 2004-123401/12.
DR N-PSDB; ADJ77815.
XX
XX New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
PT unglycosylated in its native form or for synthesizing glycolipids.
XX
PS Claim 16; SEQ ID NO 8; 72pp; English.
XX
CC This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesise glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar, as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 19C2 FutB protein sequence of the invention.
XX
SQ Sequence 277 AA;
Query Match 15.2%; Score 68; DB 8; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.5e-57;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 132
|||||
DB 74 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 133
|||||

QY 133 AESVNDTT 140
|||||
DB 134 AESVNDTT 141
|||||

RESULT 5
ADJ27351
ID ADJ27351 standard; protein; 277 AA.
XX
AC ADJ27351;
XX
DT 20-MAY-2004 (first entry)
XX
DE Alpha-1,3/4-fucosyltransferase coding sequence.
XX
KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
KW fucosyl; fucose.
XX
OS Helicobacter pylori; strain 19C2 FutB.
XX
PN WO2004009793-A2.
XX
PD 29-JAN-2004.
XX
PF 23-JUL-2003; 2003WO-US023155.
XX
PR 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Johnson KF, Bezila DJ;
XX
DR WPI; 2004-132958/13.
DR N-PSDB; ADJ27350.
XX
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX
PS Claim 1; Fig 4; 84pp; English.
XX
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX
SQ Sequence 277 AA;
Query Match 15.2%; Score 68; DB 8; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.5e-57;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 132
|||||
DB 74 NPLGSARKILSYQNAKRVFTGTGENEVPNLFDAIGFDELDFRDRLRMPLYYDLRLHHK 133
|||||

QY 133 AESVNDTT 140
|||||
DB 134 AESVNDTT 141
|||||

RESULT 6
AEB70137


```
DR WPI; 2004-132958/13.
DR N-PSDB; ADJ27344.
XX
PT Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX
PS Claim 1; Fig 1; 84pp; English.
XX
CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX
SQ Sequence 486 AA;

  Query Match      13.2%; Score 59; DB 8; Length 486;
  Best Local Similarity 100.0%; Pred. No. 1.6e-48;
  Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 DDLRVNDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYERLLQNASPLLELSQNT 424
DB 400 DDLRVNDDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYERLLQNASPLLELSQNT 458

RESULT 9
AEB70131
ID AEB70131 standard; protein; 486 AA.
XX
AC AEB70131;
XX
DT 06-OCT-2005 (first entry)
XX
DE Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 2.
XX
KW Fucosyltransferase; protein production; enzyme.
XX
OS Helicobacter pylori; strain 1182.
XX
PN US2005164338-A1.
XX
PD 28-JUL-2005.
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX
WPI; 2005-521417/53.
XX
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Disclosure; SEQ ID NO 2; 97pp; English.
XX
CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase (amino acids 1-245)
CC protein fragment.
XX
SQ Sequence 245 AA;

  Query Match      12.1%; Score 54; DB 9; Length 245;
  Best Local Similarity 100.0%; Pred. No. 6.6e-44;
  Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSARKILSYONAKRVFTGTGENVPNPNLFDYAGFDELDFDRYLRMPPLY 126
DB 72 NPLGSARKILSYONAKRVFTGTGENVPNPNLFDYAGFDELDFDRYLRMPPLY 125

RESULT 11
AEB70195
ID AEB70195 standard; protein; 391 AA.
XX
AC AEB70195;
XX
DT 06-OCT-2005 (first entry)
XX
```

DE H. pylori fucosyl transferase, FutA, protein fragment, SEQ ID NO: 66.
XX Fucosyltransferase; protein production; enzyme.
KW Helicobacter pylori; strain 1111.
XX US2005164338-A1.
PN 28-JUL-2005.
PD
XX 22-JAN-2004; 2004US-00764212.
XX 22-JAN-2004; 2004US-00764212.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA (UYAL-) UNIV ALBERTA.
XX Simaia-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
DR New isolated fucosyltransferase polynucleotides and polypeptides, useful
XX for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX Disclosure; SEQ ID NO 66; 97pp; English.
XX The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase catalytic domain
CC (amino acids 27-417) protein fragment.
XX Sequence 391 AA;
SQ
Query Match 12.1%; Score 54; DB 9; Length 391;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 NPLGSARKILSYQNAKRVFTYTGNEVNFNFDFYAIAGDFDELDFRDYLRMPLYY 126
Db 46 NPLGSARKILSYQNAKRVFTYTGNEVNFNFDFYAIAGDFDELDFRDYLRMPLYY 99
RESULT 12
ADJ77812
ID ADJ77812 standard; protein; 432 AA.
XX ADJ77812;
AC
XX 06-MAY-2004 (first entry)
DT
XX Helicobacter pylori strain 1111 FutA protein SeqID 4.
DE
XX FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
XX fucose; N-acetylglucosamine; glycoconjugate; enzyme.
KW
KW Helicobacter pylori.
OS
XX WO2004009838-A2.
XX 29-JAN-2004.
PN
XX 23-JUL-2003; 2003WO-US023057.
XX 23-JUL-2003; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
PR
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA
XX Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX N-PSDB; ADJ27346.
DR
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX Claim 1; Fig 2; 84pp; English.
PS
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which

XX WPI; 2004-123401/12.
DR N-PSDB; ADJ77811.
XX New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
PT unglycosylated in its native form or for synthesizing glycolipids.
XX Claim 16; SEQ ID NO 4; 72pp; English.
PS
XX This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesise glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 1111 FutA protein sequence of the invention.
XX Sequence 432 AA;
SQ
Query Match 12.1%; Score 54; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 NPLGSARKILSYQNAKRVFTYTGNEVNFNFDFYAIAGDFDELDFRDYLRMPLYY 126
Db 72 NPLGSARKILSYQNAKRVFTYTGNEVNFNFDFYAIAGDFDELDFRDYLRMPLYY 125
RESULT 13
ADJ27347
ID ADJ27347 standard; protein; 432 AA.
XX AC ADJ27347;
XX 20-MAY-2004 (first entry)
DT
XX Alpha-1,3/4-fucosyltransferase.
DE
XX alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
KW fucosyl; fucose.
KW
XX Helicobacter pylori; strain 1111 FutA.
OS
XX WO2004009793-A2.
XX 29-JAN-2004.
PN
XX 23-JUL-2003; 2003WO-US023155.
XX 23-JUL-2002; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
PR
XX (NEOS-) NEOSE TECHNOLOGIES INC.
PA
XX Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX N-PSDB; ADJ27346.
DR
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX Claim 1; Fig 2; 84pp; English.
PS
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which

CC was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.

XX Sequence 432 AA;

SQ Query Match 12.1%; Score 54; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSAKILSYQNAKRVFTYTGNEVPNFNLDYVIGFDELDLDRDRLRMLPLY 126
Db 72 NPLGSAKILSYQNAKRVFTYTGNEVPNFNLDYVIGFDELDLDRDRLRMLPLY 125

RESULT 14

ABE70133 ID ABE70133 standard; protein; 432 AA.

AC ABE70133;

DT 06-OCT-2005 (first entry)

XX Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 4.

DE Fucosyltransferase; protein production; enzyme.

XX Helicobacter pylori; strain 1111.

OS US2005164338-A1.

XX 28-JUL-2005.

XX 22-JAN-2004; 2004US-00764212.

XX 22-JAN-2004; 2004US-00764212.

PA (NEOS-) NEOSE TECHNOLOGIES INC.

PA (UVAL-) UNIV ALBERTA.

PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;

XX WPI; 2005-521417/53.

DR N-PSDB; ABE70132.

XX New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

PS Example 1; SEQ ID NO 4; 97pp; English.

XX The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

XX Sequence 432 AA;

SQ Query Match 12.1%; Score 54; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSAKILSYQNAKRVFTYTGNEVPNFNLDYVIGFDELDLDRDRLRMLPLY 126
Db 72 NPLGSAKILSYQNAKRVFTYTGNEVPNFNLDYVIGFDELDLDRDRLRMLPLY 125

RESULT 15

ABU52257

ID ABU52257 standard; protein; 418 AA.

XX ABU52257;

DT 07-MAY-2003 (first entry)

XX Helicobacter pylori selected interacting domain (SID) protein #1601.

XX Protein-protein interaction; ulcer; selected interacting domain; SID.

OS Helicobacter pylori.

XX WO200266501-A2.

PD 29-AUG-2002.

XX 28-DEC-2001; 2001WO-BP015428.

XX 02-JAN-2001; 2001US-0259302P.

XX (HYBR-) HYBRIGENICS.

PA (INSP) INST PASTEUR.

XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;

XX WPI; 2002-674910/72.

DR N-PSDB; ABX67002.

XX New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.

XX Claim 6; Page 479; 642pp; English.

XX The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue

XX Sequence 418 AA;

SQ Query Match 11.9%; Score 53; DB 5; Length 418;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 NKSEFLSOYKFNLCFNSQGYGVTEKILDAYFESHHTPIYWGSPSVAKDNPK 276

Db 218 NKSEFLSOYKFNLCFNSQGYGVTEKILDAYFESHHTPIYWGSPSVAKDNPK 270

Search completed: August 11, 2006, 20:00:03

Job time : 118.313 secs

GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:00:25 ; Search time 20.9374 Seconds
(without alignments)
2049.570 Million cell updates/sec

Title: US-10-764-212-16
Perfect score: 446
Sequence: 1 MFQPLLDAYVESIEKMAS.....KIYKAYQKPIKNPYPYCAP 446

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	11.9	425	2	C64567 fucosyltransferase
2	53	11.9	476	2	C64601 fucosyltransferase
3	46	10.3	436	2	G71862 alpha-(1,3)-fucosyl
4	46	10.3	454	2	B71914 alpha-(1,3)-fucosyl
5	9	2.0	667	2	T09482 ring finger protein
6	8	1.8	318	2	T11260 NADH2 dehydrogenas
7	8	1.8	551	2	S18408 alkaline phosphata
8	8	1.8	559	2	B36307 alkaline phosphata
9	8	1.8	1007	2	S48535 rho-type GTPase-ac
10	8	1.8	1139	2	B4962 sterol regulatory
11	8	1.8	1141	2	A54962 sterol regulatory
12	8	1.8	1409	1	OrFFCP copia polyprotein
13	8	1.8	3343	2	S44887 ZK112.7 protein -
14	7	1.6	71	2	B82791 conserved hypothet
15	7	1.6	79	2	T10336 conserved hypothet
16	7	1.6	92	2	T18728 conserved hypothet
17	7	1.6	139	2	F97095 integral membrane
18	7	1.6	152	2	C97249 probable nucleotid
19	7	1.6	154	2	B82457 conserved hypothet
20	7	1.6	162	2	H97620 conserved hypothet
21	7	1.6	162	2	AG2843 conserved hypothet
22	7	1.6	173	2	H84992 shikimate kinase (
23	7	1.6	173	2	AC1000 shikimate kinase (
24	7	1.6	173	2	AD0019 shikimate kinase (
25	7	1.6	174	2	G83712 shikimate kinase (
26	7	1.6	215	2	B84078 conserved hypothet
27	7	1.6	219	2	AF1320 conserved hypothet
28	7	1.6	219	2	AF1692 conserved hypothet
29	7	1.6	222	2	G86717 conserved hypothet

30	7	1.6	228	2	C69859 two-component resp
31	7	1.6	240	1	A65134 shikimate kinase (
32	7	1.6	240	2	H91157 shikimate kinase I
33	7	1.6	240	2	F86003 shikimate kinase I
34	7	1.6	244	2	C96796 probable heat shoc
35	7	1.6	267	2	T22978 hypothetical prote
36	7	1.6	268	2	C90566 hypothetical prote
37	7	1.6	290	2	T34443 hypothetical prote
38	7	1.6	304	2	D71290 probable ATP-bindi
39	7	1.6	319	2	AH3527 D-xylose-binding p
40	7	1.6	327	2	T41198 probable thiamin b
41	7	1.6	336	2	H84767 probable peroxidase
42	7	1.6	341	2	G82014 dTDPglucose 4,6-de
43	7	1.6	351	2	S07407 peroxidase (EC 1.1
44	7	1.6	352	1	BVECHD molybdenum transpo
45	7	1.6	352	2	AE0595 molybdenum.transpo

ALIGNMENTS

RESULT 1

C64567 fucosyltransferase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64567
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64567
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <TOM>
A:Cross-references: UNIPROT:O25142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID:

Query Match	11.9%	Score 53;	DB 2;	Length 425;
Best Local Similarity	100.0%;	Pred. No. 1.2e-48;		
Matches 53;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	224	NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPK	276	
Db	225	NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPK	277	

RESULT 2

C64601 fucosyltransferase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64601
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64601
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-476 <TOM>
A:Cross-references: UNIPROT:O25366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID:

Query Match	11.9%	Score 53;	DB 2;	Length 476;
Best Local Similarity	100.0%;	Pred. No. 1.4e-48;		
Matches 53;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	224	NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPK	276	

Db 225 NKSEFLSYKFNLCFENSQGYVTEKILDAYPSTHTPIYWGSPVAKDFNPK 277
|||||

RESULT 3

G71862
alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <ARN>
A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000D36D2; GB:AE001439; NID
A;Experimental source: strain J99

Query Match 10.3%; Score 46; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.7e-41;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 RNAYDALNSIEPTVGGSVKNTLGYNNKNSBFLSQYKFNLCFEN 240
|||||

Db 195 RNAYDALNSIEPTVGGSVKNTLGYNNKNSBFLSQYKFNLCFEN 240
|||||

RESULT 4

B71914
alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <ARN>
A;Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: fuct

Query Match 10.3%; Score 46; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.9e-41;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 RNAYDALNSIEPTVGGSVKNTLGYNNKNSBFLSQYKFNLCFEN 240
|||||

Db 195 RNAYDALNSIEPTVGGSVKNTLGYNNKNSBFLSQYKFNLCFEN 240
|||||

RESULT 5

T09482
ring finger protein FXV - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16687
A;Accession: T09482

A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-667 <PER>
A;Cross-references: UNIPROT:O15344; UNIPARC:UPI000012F0E6; EMBL:AF035360; NID:G2827993; I
C;Genetics:
A;Gene: FXV
A;Map position: Xp22.3
C;Superfamily: rfp transforming protein
P;6-65/Domain: RING finger homology <RRN>

Query Match 2.0%; Score 9; DB 2; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 AFYDALNSI 205
|||||

Db 616 AFYDALNSI 624
|||||

RESULT 6

T11260
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - hardbacked tick (Ix
C:Species: mitochondrion Ixodes hexagonus
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11260
R;Black IV, W.C.; Roehrdanz, R.L.
Mol. Biol. Evol. 15, 1772-1785, 1998
A>Title: Mitochondrial gene order is not conserved in arthropods: prostriate and metastri
A;Reference number: Z17252; MUID:99083443; PMID:9866211
A;Accession: T11260
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-318 <BLA>
A;Cross-references: UNIPROT:O99805; UNIPARC:UPI00000976B1; EMBL:AF081828; NID:G4164542; I
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 1.8%; Score 8; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 SPKKILAF 334
|||||

Db 154 SPKKILAF 161
|||||

RESULT 7

S18408
alkaline phosphatase (EC 3.1.3.1) - rat
N;Alternate names: phytase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: S18408; S17576
R;Strom, M.; Kisinger, J.; DeLuca, H.F.
Biochim. Biophys. Acta 1090, 293-304, 1991
A>Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg
A;Reference number: S18408; MUID:92062729; PMID:1954251
A;Accession: S18408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-551 <STR>
A;Cross-references: UNIPROT:P51740; UNIPARC:UPI0000132000
A;Note: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c
R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
A>Title: Purification and characterization of phytase from rat intestinal mucosa.
A;Reference number: S17576; MUID:91370007; PMID:1654110
A;Accession: S17576
A;Molecule type: protein
A;Residues: 20-29 <YAN>
A;Cross-references: UNIPARC:UPI00000E5C7D

RESULT 8

S18408
alkaline phosphatase (EC 3.1.3.1) - rat
N;Alternate names: phytase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: S18408; S17576
R;Strom, M.; Kisinger, J.; DeLuca, H.F.
Biochim. Biophys. Acta 1090, 293-304, 1991
A>Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg
A;Reference number: S18408; MUID:92062729; PMID:1954251
A;Accession: S18408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-551 <STR>
A;Cross-references: UNIPROT:P51740; UNIPARC:UPI0000132000
A;Note: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c
R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
A>Title: Purification and characterization of phytase from rat intestinal mucosa.
A;Reference number: S17576; MUID:91370007; PMID:1654110
A;Accession: S17576
A;Molecule type: protein
A;Residues: 20-29 <YAN>
A;Cross-references: UNIPARC:UPI00000E5C7D

A>Note: 10-Val was also found
C:Superfamily: Alkaline phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 1.8%; Score 8; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 PLNALDGK 319
|||||
DB 398 PLNALDGK 405

RESULT 8

B36307
alkaline phosphatase (EC 3.1.3.1), intestinal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004
C:Accession: B36307
R:Manes, T.; Glade, K.; Ziomek, C.A.; Millan, J.L.
Genomics 8, 541-554, 1990
A:Title: Genomic structure and comparison of mouse tissue-specific alkaline phosphatase
A:Reference number: A36307; MUID:91139124; PMID:2286375
A:Accession: B36307
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-559 <MAN>
A:Cross-references: UNIPROT:P24822; UNIPARC:UPI000002749A; GB:M61705; NID:gl94048; PID:N
C:Superfamily: Alkaline phosphatase
C:Keywords: intestine; phosphoprotein; phosphoric monoester hydrolase

Query Match 1.8%; Score 8; DB 2; Length 559;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 PLNALDGK 319
|||||
DB 398 PLNALDGK 405

RESULT 9

S48535
rho-type GTPase-activating protein DBM1 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G3290; protein YOR127w; protein YOR3290w
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: S48535; S60987; S61683; S67012; S63864; JC6097
R:Chen, G.; Zheng, L.; Chan, C.S.M.
submitted to the EMBL Data Library, March 1994
A:Description: Molecular characterization of Dbm1, a novel rhoGAP protein in yeast.
A:Reference number: S48535
A:Accession: S48535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1007 <CHE>
A:Cross-references: UNIPROT:P39083; UNIPARC:UPI0000133814; EMBL:U07421; NID:g460972; PID
R:Wiemann, S.; Rechmann, S.; Benes, V.; Voss, H.; Schwager, C.; Vlcek, C.; Stegemann, J.
submitted to the EMBL Data Library, August 1995
A:Description: Sequencing of 51 kilobases on the right arm of chromosome XV from S. cere
A:Reference number: S60983
A:Accession: S60987
A:Molecule type: DNA
A:Residues: 1-1007 <WIE>
A:Cross-references: UNIPARC:UPI0000133814; EMBL:X90518; NID:g1050808; PID:g1050813
R:Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia
submitted to the EMBL Data Library, December 1995
A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A:Reference number: S61643
A:Accession: S61683
A:Molecule type: DNA
A:Residues: 1-1007 <BEN>
A:Cross-references: UNIPARC:UPI0000133814; EMBL:X94335; NID:g1262139; PID:e217748; PID:g

R:Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoerge, W.
submitted to the Protein Sequence Database, July 1996

A:Reference number: S66965

A:Accession: S67012

A:Molecule type: DNA

A:Residues: 1-1007 <VOS>

A:Cross-references: UNIPARC:UPI0000133814; EMBL:Z75035; MIPS:YOR127w; NID:gl420329; PID:gl
A:Experimental source: strain S288C
R:Wiemann, S.; Rechmann, S.; Benes, V.; Voss, H.; Schwager, C.; Vlcek, C.; Stegemann, J.;
Yeast 12, 281-288, 1996
A:Title: Sequencing and analysis of 51 kb on the right arm of chromosome XV from Sacchar
A:Reference number: S63860; MUID:97060020; PMID:8904341

A:Accession: S63864

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1007 <WIV>

A:Cross-references: UNIPARC:UPI0000133814; EMBL:X90518; NID:g1050808; PID:g1050813
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R:Chen, G.; Zheng, L.; Chan, C.S.M.
Mol. Cell. Biol. 16, 1376-1390, 1996

A:Title: The LIM domain-containing Dbm1 GTPase-activating protein is required for normal

A:Reference number: JC6097; MUID:96239492; PMID:8657111

A:Accession: JC6097

A:Molecule type: DNA

A:Residues: 1-1007 <CHF>

A:Cross-references: UNIPARC:UPI0000133814; GB:U07421; NID:g460972; PID:g460973

A:Status: preliminary

C:Genetics:

A:Gene: SGD:RGAL; DBM1; THE1

A:Cross-references: MIPS:YOR127w; SGD:S0005653

A:Map position: 15R

A:Note: YOR127w

F:13-66/Domain: LIM metal-binding repeat homolog <LIM2>

Query Match 1.8%; Score 8; DB 2; Length 1007;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 QNPNEFSD 68
|||||
DB 754 QNPNEFSD 761

RESULT 10

B54962
sterol regulatory element binding protein 2 precursor - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: B54962
R:Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A:Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that t;
A:Reference number: A54962; MUID:95047343; PMID:7958866
A:Accession: B54962
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1139 <YAN>
A:Cross-references: UNIPROT:O60429; UNIPARC:UPI0000178926; GB:U12330
A:Note: 493 Ser was also found
C:Superfamily: sterol regulatory element binding protein
C:Keywords: DNA binding; membrane protein

Query Match 1.8%; Score 8; DB 2; Length 1139;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AIDYIKYL 297
|||||
DB 371 AIDYIKYL 378

RESULT 11

A54962
sterol regulatory element binding protein 2 precursor - human
N:Alternate names: basic-helix-loop-helix-leucine zipper transcription factor SREBP-2
C:Species: Homo sapiens (man)

C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49397; A54962
R;Hua, X.; Yokoyama, C.; Wu, J.; Briggs, M.R.; Brown, M.S.; Goldstein, J.L.; Wang, X.
Proc. Natl. Acad. Sci. U.S.A. 90, 11603-11607, 1993
A;Title: SREBP-2, a second basic-helix-loop-helix-leucine zipper protein that stimulates
A;Reference number: A49397; MUID:94089681; PMID:7903453
A;Accession: A49397
A;Molecule type: mRNA
A;Residues: 1-1141 <HUA>
A;Cross-references: UNIPROT:Q12772; UNIPARC:UPI000003269D; GB:U02031; NID:g451329; PIDN:
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:140987)
R;Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A;Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that b
A;Reference number: A54962; MUID:95047343; PMID:7958866
A;Contents: annotation
C;Comment: Under conditions of sterol depletion, this membrane-bound transcription facto
C;Genetics:
A;Gene: GDB:SREBP2; SREBP2
A;Cross-references: GDB:273625
A;Map position: Xq24-Xqter
C;Superfamily: sterol regulatory element binding protein
C;Keywords: DNA binding; membrane protein; transcription factor

Query Match 1.8%; Score 8; DB 2; Length 1141;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 AIDYIKYL 297
Db 373 AIDYIKYL 380
|||||||

RESULT 12
OFFPCP
copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia
N;Contains: copia protein, 31k; copia protein, 48K; proteinase
C;Species: Drosophila melanogaster
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A03324; S03612; S14835
R;Mount, S.M.; Rubin, G.M.
Mol. Cell. Biol. 5, 1630-1638, 1985
A;Title: Complete nucleotide sequence of the Drosophila transposable element copia: homo
A;Reference number: A03324; MUID:85267679; PMID:2410772
A;Accession: A03324
A;Molecule type: DNA
A;Residues: 1-1409 <MOU>
A;Cross-references: UNIPROT:P04146; UNIPARC:UPI0000127EE3; GB:M11240; NID:g158615; PIDN:
R;Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
Nucleic Acids Res. 17, 2134, 1989
A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A;Reference number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612
A;Molecule type: mRNA
A;Residues: 1-391,1375-1409 <MIL>
A;Cross-references: UNIPARC:UPI000002A70E; EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:
R;Yoshioaka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
EMBO J. 9, 535-541, 1990
A;Title: Virus-like particle formation of Drosophila copia through autocatalytic process
A;Reference number: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835
A;Molecule type: DNA
A;Residues: 1-391,1375-1409 <YOS>
A;Cross-references: UNIPARC:UPI000002A70E; EMBL:X54147; NID:g7749; PIDN:CAA38086.1; PID:
C;Genetics:
A;Gene: FlyBase:copia
A;Cross-references: FlyBase:FBgn0000349
A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
C;Keywords: polyprotein; proteinase
F;2-433/Product: copia protein, 48K #status predicted <MAT1>
F;2-270/Product: copia protein, 31K #status predicted <MAT2>

F;271-433/Product: proteinase #status predicted <MAT3>
Query Match 1.8%; Score 8; DB 1; Length 1409;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 PPLKIAVA 31
Db 314 PPLKIAVA 321
|||||||

RESULT 13
S44887
ZK112.7 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S44887
R;Du, Z.
submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK112.
A;Reference number: S44616
A;Accession: S44887
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3343 <DUZ>
A;Cross-references: UNIPROT:P34616; UNIPARC:UPI000013BC7C; EMBL:L14324; NID:g289740; PID:
C;Genetics:
A;Introns: 39/1; 74/3; 122/3; 209/2; 287/3; 333/2; 489/1; 611/2; 714/1; 939/3; 1002/2; 11
C;Keywords: cytoskeleton; transmembrane protein

Query Match 1.8%; Score 8; DB 2; Length 3343;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 338 ILENDTIY 345
Db 2388 ILENDTIY 2395
|||||||

RESULT 14
B82791
conserved hypothetical protein XF0564 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82791
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82791
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <SIM>
A;Cross-references: UNIPROT:Q9PTU3; UNIPARC:UPI0001368FF; GB:AE003903; GB:AE003849; NID:
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorriy, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.B.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0564

Query Match 1.6%; Score 7; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 IKEFKKS 45
DB 36 IKEFKKS 42

RESULT 15

T10336
Hypothetical protein 67 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10336
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A>Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10336
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-79 <AHR>
A:Cross-references: UNIPROT:O10321; UNIPARC:UPI000006182F; EMBL:U75930; NID:g2934903; PI

Query Match 1.6%; Score 7; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 EKILDAY 255
DB 9 EKILDAY 15

Search completed: August 11, 2006, 20:09:17
Job time : 22.9374 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:54:19 ; Search time 157.197 Seconds
(without alignments)
2624.463 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 446

Sequence: 1 MFQPLLDAVESASTKMAS.....KIYKAYQKPIKNPPYPYCAP 446

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	11.9	425	2	O25142 HELPY
2	53	11.9	476	2	O25366 HELPY
3	50	11.2	432	2	O6ST35 HELPY
4	50	11.2	462	2	O9L8S4 HELPY
5	46	10.3	436	2	O9ZKD7 HELPY
6	46	10.3	454	2	O9ZLI3 HELPY
7	43	9.6	478	2	O30511 HELPY
8	29	6.5	333	2	O32631 HELPY
9	9	2.0	34	2	O4ZCF8 9CAUD
10	9	2.0	34	2	O4ZCUB 9CAUD
11	9	2.0	94	2	O80Z72 MUSCA
12	9	2.0	94	2	O80Z75 MUSCA
13	9	2.0	94	2	O80Z78 9MURI
14	9	2.0	94	2	O80Z81 ARVTE
15	9	2.0	94	2	O80ZB5 MUSPL
16	9	2.0	94	2	O810Y0 MUSSI
17	9	2.0	108	1	TR118 MUSCR
18	9	2.0	667	1	TR118 HUMAN
19	9	2.0	667	1	TR118 MUSSP
20	9	2.0	667	1	TR118 RAT
21	8	1.8	96	2	O80410 CARPL
22	8	1.8	98	2	O7P851 FUSNI
23	8	1.8	143	2	O8SXF7 DROME
24	8	1.8	147	2	O9MYT6 PIG
25	8	1.8	147	2	O9MYT7 RABIT
26	8	1.8	147	2	O918H7 CHICK
27	8	1.8	153	2	O8SXG4 DROME
28	8	1.8	165	2	O35KX5 9BRAD
29	8	1.8	167	2	O7MAB0 WOLSU
30	8	1.8	177	2	O4SIM3 TETNG
31	8	1.8	186	2	O63FD7 BACCCZ

32	8	1.8	186	2	O6HNV7 BACHK
33	8	1.8	186	2	O81UK3 BACAN
34	8	1.8	198	2	O7TSU8 MOUSE
35	8	1.8	204	2	O6RSW5 PIG
36	8	1.8	215	2	O9Z3Z9 PSEPU
37	8	1.8	252	2	O9ESZ4 MOUSE
38	8	1.8	273	2	O9ZXM4 9CAUD
39	8	1.8	300	2	O8FU16 COREF
40	8	1.8	318	2	O99805 IXOHE
41	8	1.8	323	2	O7Q403 ANOGA
42	8	1.8	357	2	O3B3G6 PELID
43	8	1.8	359	2	O7VFA1 HELHP
44	8	1.8	360	2	O36JW3 MARHY
45	8	1.8	364	2	O44EK1 CHRSL

ALIGNMENTS

RESULT 1
O25142 HELPY PRELIMINARY; PRT; 425 AA.
AC O25142;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Fucosyltransferase.
GN OrderedLocustNames=HP0379; ORFNames=HP_0379;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.B., Dodson R.J., Khatak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.P., Fujii C., Bowman C.,
RA Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter pylori."
RL Nature 388:539-547(1997).
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CC -----
DR EMBL; AF000511; AAD07447.1; -; Genomic_DNA.
DR PIR; C64567; C64567.
DR TIGR; HP0379; -.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0008417; F: fucosyltransferase activity; IEA.
DR GO; GO:0016757; F: transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0005486; P: protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;

Query Match 11.9%; Score 53; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 5e-45; 0; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0;

QY	224	NKSEFLSQKFNLCFNSQGYGVTEKILDVFSHTPIYWGSPSVAKDNPX	276
Db	225	NKSEFLSQKFNLCFNSQGYGVTEKILDVFSHTPIYWGSPSVAKDNPX	277

```

RESULT 2
O25366_HELPY PRELIMINARY; PRT; 476 AA.
ID O25366_HELPY
AC O25366;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Fucosyltransferase.
GN OrderedLocustNames=HP0651; ORFNames=HP_0651;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.P., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
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CC
EMBL; AE000511; AAD07710.1; -; Genomic_DNA.
DR PIR; C64601; C64601.
DR TIGR; HP0651; -.
DR LinkHub; O25366; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans_10.
DR PANTHER; PTHR11929; Glyco trans_10; 1.
DR Complete proteome; Fucosyltransferase; Transferase.
SQ SEQUENCE 476 AA; 55927 MW; 32BFDBBD3681F74 CRC64;

Query Match 11.9%; Score 53; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.5e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 224 NKSEFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 276
Db 225 NKSEFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 277

RESULT 3
O6ST35_HELPY PRELIMINARY; PRT; 432 AA.
ID O6ST35_HELPY
AC O6ST35;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Alpha-1,4 fucosyltransferase.
GN Name=fucTIII;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 6709;
RX PubMed=16000696; DOI=10.1093/glycob/cwj004;
RA Rabbani S., Miksa V., Wipf B., Ernst B.;

Query Match 11.9%; Score 53; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.5e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 224 NKSEFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 276
Db 225 NKSEFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 277

RESULT 4
O9L8S4_HELPY PRELIMINARY; PRT; 462 AA.
ID O9L8S4_HELPY
AC O9L8S4;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 2.
DT 07-FEB-2006, entry version 17.
DE Alpha-1,3/4-fucosyltransferase.
GN Name=fucTa;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RX MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RT "Cloning and characterization of the alpha(1,3/4) fucosyltransferase
RT of Helicobacter pylori.";
RL J. Biol. Chem. 275:4988-4994(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans_10.
DR PANTHER; PTHR11929; Glyco trans_10; 1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;

Query Match 11.2%; Score 50; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-42;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 227 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 276
Db 225 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 274

"Molecular Cloning and Functional Expression of a Novel Helicobacter
pylori [alpha]-1,4 Fucosyltransferase.";
Glycobiology 15:1076-1083(2005).
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CC
EMBL; AY450598; AAR88243.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans_10.
DR PANTHER; PTHR11929; Glyco trans_10; 1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;

Query Match 11.2%; Score 50; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.2e-42;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 227 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 276
Db 223 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 272

RESULT 4
O9L8S4_HELPY PRELIMINARY; PRT; 462 AA.
ID O9L8S4_HELPY
AC O9L8S4;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 2.
DT 07-FEB-2006, entry version 17.
DE Alpha-1,3/4-fucosyltransferase.
GN Name=fucTa;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RX MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RT "Cloning and characterization of the alpha(1,3/4) fucosyltransferase
RT of Helicobacter pylori.";
RL J. Biol. Chem. 275:4988-4994(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans_10.
DR PANTHER; PTHR11929; Glyco trans_10; 1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;

Query Match 11.2%; Score 50; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-42;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 227 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 276
Db 225 EFLSQKFNLCFENSQGYGVTEKILDYFHSHTIPYWGSPSVAKDFNPK 274
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RESULT 5
Q9ZKD7_HELPJ PRELIMINARY; PRT; 436 AA.
AC Q9ZKD7_HELPJ
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.
GN Name=fucU; ORFNames=jhp_1002;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]_TaxID=85963;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
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DR EMBL; AE001439; AAD06573.1; -; Genomic_DNA.
DR PIR; G71862;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 436 AA; 50699 MW; 1DB2066A98FA61E CRC64;

Query Match 10.3%; Score 46; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 8.1e-38;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 RNAFYDALNSIEPTVGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
Db 195 RNAFYDALNSIEPTVGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240

RESULT 6
Q9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
AC Q9ZLI3_HELPJ
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.
GN Name=fucT; ORFNames=jhp_0596;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]_TaxID=85963;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
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DR EMBL; AE001439; AAD06573.1; -; Genomic_DNA.
DR PIR; G71862;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 436 AA; 50699 MW; 1DB2066A98FA61E CRC64;

Query Match 10.3%; Score 46; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 8.1e-38;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 RNAFYDALNSIEPTVGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
Db 195 RNAFYDALNSIEPTVGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240

RESULT 7
O30511_HELPY PRELIMINARY; PRT; 478 AA.
AC O30511_HELPY
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Alpha1,3-fucosyltransferase.
GN Name=fucT;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]_TaxID=210;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11639;
RX MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
RA Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.;
RT "Cloning and heterologous expression of an alpha1,3-fucosyltransferase
RT gene from the gastric pathogen Helicobacter pylori."
RL J. Biol. Chem. 272:21357-21363(1997).
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DR EMBL; AF008596; AA81031.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;

Query Match 9.6%; Score 43; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKPK 43
Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWDEEIKPK 43

RESULT 8
O32631_HELPY PRELIMINARY; PRT; 333 AA.
ID O32631_HELPY
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AC Q32631;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.1-).
GN Name=fucT;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11637;
RX MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Eijnden D.H.,
RA Bird M.I.;
RT "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
RT alpha(1,3)-fucosyltransferase gene.";
RL J. Biol. Chem. 272:21349-21356(1997).
CC -----
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CC -----
DR EMBL; AF006039; AAB93985.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; GlycoTrans I0.
DR PANTHER; PTHR11929; GlycoTrans I0; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFFCB1AC127E0A8C CRC64;

Query Match 6.5%; Score 29; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 SFVSNANAPNRNPFYDALNSIEPVTGGG 212
Db 63 SFVSNANAPNRNPFYDALNSIEPVTGGG 91
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RESULT 9
Q4ZCF8_9CAUD PRELIMINARY; PRT; 34 AA.
AC Q4ZCF8;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE ORF185.
OS Bacteriophage 47.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=320839;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 Staphylococcus aureus
RT bacteriophages";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY954957; AAX91263.1; -; Genomic DNA.
DR SEQUENCE 34 AA; 3962 MW; 348D427904DF6E16 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 RGVVSFVAS 188
Db |||||

Db 20 RGVVSFVAS 28

RESULT 10
Q4ZCUB_9CAUD PRELIMINARY; PRT; 34 AA.
AC Q4ZCUB;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE ORF191.
OS Bacteriophage 42e.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=320837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 Staphylococcus aureus
RT bacteriophages";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
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CC -----
DR EMBL; AY954955; AAX91190.1; -; Genomic DNA.
DR SEQUENCE 34 AA; 4006 MW; 263AB27910DE2E16 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 RGVVSFVAS 188
Db |||||
20 RGVVSFVAS 28

RESULT 11
Q80Z72_MUSMA PRELIMINARY; PRT; 94 AA.
AC Q80Z72;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mus macedonicus (Macedonian mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=XBS;
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RA Montoya-Burgos J.I., Bourcet P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
CC -----
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CC -----
DR EMBL; AY181231; AAO62991.1; -; Genomic DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003879; Butyrophilin.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHILNCDF.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 2.4; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 12
Q80275 MUSCE
ID Q80275 MUSCE PRELIMINARY; PRT; 94 AA.
AC Q80275, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mus cervicolor (Fawn-colored mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CRIC;
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RT Montoya-Burgos J.I., Boursot P., Galtier N.;
RL "Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 14
Q80281 ARVTE
ID Q80281 ARVTE PRELIMINARY; PRT; 94 AA.
AC Q80281;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Arvicola terrestris (European water vole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Cricetidae; Arvicolinae; Arvicola.
NCBI_TaxID=10050;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RT Montoya-Burgos J.I., Boursot P., Galtier N.;
RL "Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10633 MW; 1485630849DFB9AF CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 15
Q802B5 MUSPL
ID Q802B5 MUSPL PRELIMINARY; PRT; 94 AA.
AC Q802B5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Fxy (Fragment).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10633 MW; 1485630849DFB9AF CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 16
Q802B5 MUSPL
ID Q802B5 MUSPL PRELIMINARY; PRT; 94 AA.
AC Q802B5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Fxy (Fragment).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10633 MW; 1485630849DFB9AF CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 17
Q80278 MURI
ID Q80278 MURI PRELIMINARY; PRT; 94 AA.
AC Q80278;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mastomys huberti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mastomys.
NCBI_TaxID=121569;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RT Montoya-Burgos J.I., Boursot P., Galtier N.;
RL "Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 18
Q80278 MURI
ID Q80278 MURI PRELIMINARY; PRT; 94 AA.
AC Q80278;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mastomys huberti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mastomys.
NCBI_TaxID=121569;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RT Montoya-Burgos J.I., Boursot P., Galtier N.;
RL "Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).

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EMBL; AY181228; AAO62988.1; -; Genomic_DNA.
InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophilin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHLNCDUF.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
DB 55 AFYDALNSI 63

RESULT 19
Q80278 MURI
ID Q80278 MURI PRELIMINARY; PRT; 94 AA.
AC Q80278;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mastomys huberti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mastomys.
NCBI_TaxID=121569;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RT Montoya-Burgos J.I., Boursot P., Galtier N.;
RL "Recombination explains isochores in mammalian genomes."; Trends Genet.

OS Mus platythrix (Flat-haired mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10101;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RC STRAIN=PTX;
 RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
 RA Montoya-Burgos J.I., Boursot P., Galtier N.;
 RT "Recombination explains isochores in mammalian genomes."
 RL Trends Genet. 19:128-130(2003).
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 CC -----
 DR EMBL; AY181234; AA053222.1; -; Genomic_DNA.
 DR InterPro; IPR001870; B302.
 DR InterPro; IPR003879; Butyrophilin.
 DR InterPro; IPR003877; SPRY_rcpt.
 DR Pfam; PF00622; SPRY; 1.
 DR PRINTS; PR01407; BUTYPHLNCDUF.
 FT NON TER 1
 FT NON TER 94
 SQ SEQUENCE 94 AA; 10587 MW; 123565BEP9C7084F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred.No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 197 AFYDALNSI 205
 Db |||||
 55 AFYDALNSI 63

Search completed: August 11, 2006, 20:08:10
 Job time : 159.197 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
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2	59	13.2	486	2	US-09-733-528A-2	Sequence 2, Appli
3	59	13.2	486	2	US-10-189-977A-2	Sequence 2, Appli
4	59	13.2	486	3	US-10-392-098A-2	Sequence 2, Appli
5	53	11.9	425	2	US-09-092-315-6	Sequence 6, Appli
6	53	11.9	425	2	US-09-733-524A-6	Sequence 6, Appli
7	53	11.9	425	2	US-10-189-977A-6	Sequence 6, Appli
8	53	11.9	425	3	US-10-392-098A-6	Sequence 6, Appli
9	53	11.9	476	2	US-09-092-315-5	Sequence 5, Appli
10	53	11.9	476	2	US-09-733-524A-5	Sequence 5, Appli
11	53	11.9	476	2	US-10-189-977A-5	Sequence 5, Appli
12	53	11.9	476	3	US-10-392-098A-5	Sequence 5, Appli
13	43	9.6	372	2	US-09-092-315-13	Sequence 13, Appli
14	43	9.6	464	2	US-09-092-315-1	Sequence 1, Appli
15	43	9.6	464	2	US-09-733-524A-1	Sequence 1, Appli
16	43	9.6	464	2	US-10-189-977A-1	Sequence 1, Appli
17	43	9.6	464	3	US-10-392-098A-1	Sequence 1, Appli
18	43	9.6	478	2	US-09-092-315-7	Sequence 7, Appli
19	43	9.6	478	2	US-09-733-524A-7	Sequence 7, Appli
20	43	9.6	478	2	US-10-189-977A-7	Sequence 7, Appli
21	43	9.6	478	3	US-10-392-098A-7	Sequence 7, Appli
22	42	9.4	454	2	US-09-092-315-8	Sequence 8, Appli
23	42	9.4	454	2	US-09-733-524A-8	Sequence 8, Appli
24	42	9.4	454	2	US-10-189-977A-8	Sequence 8, Appli
25	42	9.4	454	3	US-10-392-098A-8	Sequence 8, Appli
26	26	5.8	440	2	US-09-092-315-3	Sequence 3, Appli


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Query Match      11.9%; Score 53; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
    |||||
Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

RESULT 7
US-10-189-977A-6
; Sequence 6, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-6

Query Match      11.9%; Score 53; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

RESULT 8
US-10-392-098A-6
; Sequence 6, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695B

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; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-6

Query Match      11.9%; Score 53; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
    |||||
Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

RESULT 9
US-09-092-315-5
; Sequence 5, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-5

Query Match      11.9%; Score 53; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

RESULT 10
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match      11.9%; Score 53; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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Db 225 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPK 277

RESULT 11

US-10-189-977A-5

; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-5

Query Match 11.9%; Score 53; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-42; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0;

Qy 224 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPK 276

Db 225 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPK 277

RESULT 12

US-10-392-098A-5

; Sequence 5, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1.3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpPuct)
US-10-392-098A-5

Query Match 11.9%; Score 53; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-42; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0;

Qy 224 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPK 276
Db 225 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPK 277

RESULT 13

US-09-092-315-13
; Sequence 13, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-13

Query Match 9.6%; Score 43; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8e-33;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLLDAYVESASTEKMASKSPPLKTIYAVANNWGDDEIKKPK 43

Db 1 MFQPLLDAYVESASTEKMASKSPPLKTIYAVANNWGDDEIKKPK 43

RESULT 14

US-09-092-315-1
; Sequence 1, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-1

Query Match 9.6%; Score 43; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 9.6e-33;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLLDAYVESASTEKMASKSPPLKTIYAVANNWGDDEIKKPK 43

Db 1 MFQPLLDAYVESASTEKMASKSPPLKTIYAVANNWGDDEIKKPK 43

RESULT 15

US-09-733-524A-1
; Sequence 1, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming

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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-1

Query Match
Best Local Similarity 9.6%; Score 43; DB 2; Length 464;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWGDEIKKPK 43
Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWGWGDEIKKPK 43

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Search completed: August 11, 2006, 20:10:51
Job time : 31.9076 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:09:35 ; Search time 107.678 Seconds
(without alignments)
1918.625 Million cell updates/sec

Title: US-10-764-212-16
Perfect score: 446
Sequence: 1 MFQPLLDAYVESASIEKMAS.....KIYKAYQKINPPYPYCAP 446

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	446	5	US-10-764-212-16 Sequence 16, Appl
2	68	15.2	247	5	US-10-764-212-76 Sequence 76, Appl
3	68	15.2	256	5	US-10-764-212-70 Sequence 70, Appl
4	68	15.2	277	5	US-10-764-212-8 Sequence 8, Appl
5	59	13.2	486	4	US-10-120-319-2 Sequence 2, Appl
6	59	13.2	486	4	US-10-189-977-2 Sequence 2, Appl
7	59	13.2	486	4	US-10-392-098-2 Sequence 2, Appl
8	59	13.2	486	5	US-10-764-212-2 Sequence 72, Appl
9	54	12.1	245	5	US-10-764-212-72 Sequence 66, Appl
10	54	12.1	391	5	US-10-764-212-66 Sequence 4, Appl
11	54	12.1	432	5	US-10-764-212-4 Sequence 16, Appl
12	53	11.9	424	3	US-09-733-524-16 Sequence 6, Appl
13	53	11.9	425	4	US-10-120-319-6 Sequence 6, Appl
14	53	11.9	425	4	US-10-189-977-6 Sequence 6, Appl
15	53	11.9	425	4	US-10-392-098-6 Sequence 12, Appl
16	53	11.9	425	5	US-10-764-212-12 Sequence 5, Appl
17	53	11.9	476	3	US-09-733-524-15 Sequence 5, Appl
18	53	11.9	476	4	US-10-120-319-5 Sequence 5, Appl
19	53	11.9	476	4	US-10-189-977-5 Sequence 5, Appl
20	53	11.9	476	4	US-10-392-098-5 Sequence 20, Appl
21	50	11.2	456	5	US-10-764-212-20 Sequence 64, Appl
22	48	10.8	231	5	US-10-764-212-64 Sequence 74, Appl
23	48	10.8	246	5	US-10-764-212-74 Sequence 75, Appl
24	48	10.8	246	5	US-10-764-212-75 Sequence 68, Appl
25	48	10.8	377	5	US-10-764-212-68 Sequence 2, Appl
26	48	10.8	485	3	US-09-733-524-2 Sequence 6, Appl
27	48	10.8	485	5	US-10-764-212-6

ALIGNMENTS

RESULT 1

US-10-764-212-16
; Sequence 16, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 PutB fucosyltransferase
; US-10-764-212-16

Query Match	100.0%	Score	446	DB	5	Length	446
Best Local Similarity	100.0%	Pred. No.	0	Mismatches	0	Indels	0
Matches	446	Conservative	0			Gaps	0
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Db	1	MFQPLLDAYVESASIEKMASPPPLKIAVANWGDDEEIKFKKSVLYFIFSQRYTIALH	60				
QY	61	QNPNEFSDLVFNPLGSAKILSYQNAKRVFTGGENEVPNFNFDAIGAIDELDFRDRYL	120				
Db	61	QNPNEFSDLVFNPLGSAKILSYQNAKRVFTGGENEVPNFNFDAIGAIDELDFRDRYL	120				
QY	121	RNPYYDRLHHKASVNDTTSYKLNLSLYTLKKPSHOFKENHPNLCAVNVNDESDPLKR	180				
Db	121	RNPYYDRLHHKASVNDTTSYKLNLSLYTLKKPSHOFKENHPNLCAVNVNDESDPLKR	180				
QY	181	GVVSFVSNANAPMNAFYDALNSIEPTVGGSGSVKNTLGYNVNKNKSEFSLQYKFNLCFN	240				
Db	181	GVVSFVSNANAPMNAFYDALNSIEPTVGGSGSVKNTLGYNVNKNKSEFSLQYKFNLCFN	240				
QY	241	SGQYGVVTEKILDAYFSHTPIYWGSPSVAKDFNPKFVNVNHDFFNPFDEAIDYIKYLHHT	300				
Db	241	SGQYGVVTEKILDAYFSHTPIYWGSPSVAKDFNPKFVNVNHDFFNPFDEAIDYIKYLHHT	300				
QY	301	PNAYLDMLYENPLNADGKAYFYQDLSFKKILAFFKTLILENDTIYHKSTSFWMCECLDE	360				

Sequence 8558, Ap
Sequence 8559, Ap
Sequence 61, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 18, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 77, Appl


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; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-2

Query Match      13.2%; Score 59; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 424
DB 400 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 458

RESULT 6
US-10-189-977-2
; Sequence 2, Application US/10189977
; Publication NO. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-2

Query Match      13.2%; Score 59; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 424
DB 400 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 458

RESULT 7
US-10-392-098-2
; Sequence 2, Application US/10392098
; Publication NO. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-2
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Query Match      13.2%; Score 59; DB 4; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 424
DB 400 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 458

RESULT 8
US-10-764-212-2
; Sequence 2, Application US/10764212
; Publication NO. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1182 PutB fucosyltransferase
US-10-764-212-2

Query Match      13.2%; Score 59; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 424
DB 400 DDLRVNYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVRVYERLLQNASPLLELSQNT 458

RESULT 9
US-10-764-212-72
; Sequence 72, Application US/10764212
; Publication NO. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 PutA fucosyltransferase
; OTHER INFORMATION: positions 1-245 (1111PutA.pep)
US-10-764-212-72

Query Match      12.1%; Score 54; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 73 NPLGSAKILSYQNAKRVFTTGNEVNFNLFDAIGDFDELDFDRYLRMPLYY 126
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Db 72 NPLGSAKILSYQNAKRVFTTGNEVNFNLFDAIGDFDELDFDRYLRMPLYY 125
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RESULT 10

US-10-764-212-66
; Sequence 66, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 FutA fucosyltransferase
; OTHER INFORMATION: catalytic domain conserved region positions 27-417
US-10-764-212-66

Query Match 12.1%; Score 54; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.7e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSAKILSYQNAKRVFTTGNEVNFNLFDAIGDFDELDFDRYLRMPLYY 126
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RESULT 11

US-10-764-212-4
; Sequence 4, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 FutA fucosyltransferase
US-10-764-212-4

Query Match 12.1%; Score 54; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.8e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 NPLGSAKILSYQNAKRVFTTGNEVNFNLFDAIGDFDELDFDRYLRMPLYY 126
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Db 72 NPLGSAKILSYQNAKRVFTTGNEVNFNLFDAIGDFDELDFDRYLRMPLYY 125
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RESULT 12

US-09-733-524-16
; Sequence 16, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695B
US-09-733-524-16

Query Match 11.9%; Score 53; DB 3; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
|||||
Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277
|||||

RESULT 13

US-10-120-319-6
; Sequence 6, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-6

Query Match 11.9%; Score 53; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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Db 225 NKSEFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277
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RESULT 14

US-10-189-977-6
; Sequence 6, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-6

Query Match 11.9%; Score 53; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
Db 225 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

RESULT 15
US-10-392-098-6
; Sequence 6, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-6

Query Match 11.9%; Score 53; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
Db 225 NKSEFLSQYKFNLCFENSQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277

Search completed: August 11, 2006, 20:16:20
Job time : 108.678 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:11:06 ; Search time 16.9493 Seconds
(without alignments)
1771.230 Million cell updates/sec

Title: US-10-764-212-16

Perfect score: 446

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 239914 seqs, 67312017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 239854

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Published Applications AA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.0	34	US-10-471-571A-98	Sequence 98, Appl
2	9	2.0	667	US-11-289-102-250	Sequence 250, App
3	7	1.6	149	US-10-953-349-24876	Sequence 24876, A
4	7	1.6	152	US-10-953-349-24875	Sequence 24875, A
5	7	1.6	161	US-10-953-349-6784	Sequence 6784, Ap
6	7	1.6	161	US-11-056-355B-30485	Sequence 30485, A
7	7	1.6	161	US-11-056-355B-34075	Sequence 34075, A
8	7	1.6	161	US-11-056-355B-43780	Sequence 43780, A
9	7	1.6	161	US-11-056-355B-105984	Sequence 105984, A
10	7	1.6	161	US-11-056-355B-117223	Sequence 117223, A
11	7	1.6	248	US-11-056-355B-106366	Sequence 106366, A
12	7	1.6	248	US-11-056-355B-117605	Sequence 117605, A
13	7	1.6	277	US-11-056-355B-106365	Sequence 106365, A
14	7	1.6	277	US-11-056-355B-117604	Sequence 117604, A
15	7	1.6	293	US-10-953-349-27635	Sequence 27635, A
16	7	1.6	293	US-11-056-355B-63938	Sequence 63938, A
17	7	1.6	336	US-11-056-355B-106364	Sequence 106364, A
18	7	1.6	336	US-11-056-355B-117603	Sequence 117603, A
19	7	1.6	372	US-10-953-349-23950	Sequence 23950, A
20	7	1.6	389	US-10-953-349-27634	Sequence 27634, A
21	7	1.6	389	US-11-056-355B-63937	Sequence 63937, A
22	7	1.6	418	US-10-953-349-23949	Sequence 23949, A
23	7	1.6	433	US-11-056-355B-72058	Sequence 72058, A
24	7	1.6	447	US-10-953-349-27633	Sequence 27633, A
25	7	1.6	447	US-11-056-355B-63936	Sequence 63936, A

26	7	1.6	452	7	US-11-056-355B-58710	Sequence 58710, A
27	7	1.6	462	7	US-11-056-355B-58709	Sequence 58709, A
28	7	1.6	468	7	US-11-056-355B-72057	Sequence 72057, A
29	7	1.6	469	7	US-11-056-355B-8574	Sequence 8574, Ap
30	7	1.6	469	7	US-11-056-355B-17428	Sequence 17428, A
31	7	1.6	471	7	US-11-056-355B-8573	Sequence 8573, Ap
32	7	1.6	471	7	US-11-056-355B-17427	Sequence 17427, A
33	7	1.6	479	6	US-10-953-349-23948	Sequence 23948, A
34	7	1.6	494	7	US-11-056-355B-72056	Sequence 72056, A
35	7	1.6	506	7	US-11-056-355B-58708	Sequence 58708, A
36	7	1.6	508	7	US-11-056-355B-8572	Sequence 8572, Ap
37	7	1.6	508	7	US-11-056-355B-17426	Sequence 17426, A
38	7	1.6	515	7	US-11-330-403-14952	Sequence 14952, A
39	7	1.6	516	6	US-10-953-349-31462	Sequence 31462, A
40	7	1.6	516	7	US-11-056-355B-69280	Sequence 69280, A
41	7	1.6	545	6	US-10-953-349-31461	Sequence 31461, A
42	7	1.6	545	7	US-11-056-355B-69279	Sequence 69279, A
43	7	1.6	593	6	US-10-953-349-31460	Sequence 31460, A
44	7	1.6	593	7	US-11-056-355B-69278	Sequence 69278, A
45	7	1.6	801	7	US-11-330-403-14742	Sequence 14742, A

ALIGNMENTS

RESULT 1
US-10-471-571A-98
; Sequence 98, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 98
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-471-571A-98

Query Match 2.0%; Score 9; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 RGVVSFVAS 188
Db |||||
20 RGVVSFVAS 28

RESULT 2
US-11-289-102-250
; Sequence 250, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 667

Query Match 2.0%; Score 9; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 RGVVSFVAS 188
Db |||||
20 RGVVSFVAS 28

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-250

Query Match      2.0%; Score 9; DB 7; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 AFYDALNSI 205
Db 616 AFYDALNSI 624

RESULT 3
US-10-953-349-24876
; Sequence 24876, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24876
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24876

Query Match      1.6%; Score 7; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 NVKNKSE 227
Db 32 NVKNKSE 38

RESULT 4
US-10-953-349-24875
; Sequence 24875, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24875
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24875

Query Match      1.6%; Score 7; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 NVKNKSE 227
Db 35 NVKNKSE 41

RESULT 5
US-10-953-349-6784
; Sequence 6784, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6784
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6784

Query Match      1.6%; Score 7; DB 6; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LVFSNPL 75
Db 5 LVFSNPL 11

RESULT 6
US-11-056-355B-30485
; Sequence 30485, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 30485
; LENGTH: 161
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13497623
US-11-056-355B-30485

Query Match      1.6%; Score 7; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LVFSNPL 75
Db 5 LVFSNPL 11

RESULT 7
US-11-056-355B-34075
; Sequence 34075, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
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; SEQ ID NO 34075
; LENGTH: 161
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13497623
US-11-056-355B-34075

Query Match          1.6%; Score 7; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      69 LVFSNPL 75
DB      5 LVFSNPL 11

RESULT 8
US-11-056-355B-43780
; Sequence 43780, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 43780
; LENGTH: 161
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13497623
US-11-056-355B-43780

Query Match          1.6%; Score 7; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      69 LVFSNPL 75
DB      5 LVFSNPL 11

RESULT 9
US-11-056-355B-105984
; Sequence 105984, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 105984
; LENGTH: 161
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
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; NAME/KEY: peptide
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13618494
US-11-056-355B-105984

Query Match          1.6%; Score 7; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      69 LVFSNPL 75
DB      5 LVFSNPL 11

RESULT 10
US-11-056-355B-117223
; Sequence 117223, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117223
; LENGTH: 161
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13618494
US-11-056-355B-117223

Query Match          1.6%; Score 7; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      69 LVFSNPL 75
DB      5 LVFSNPL 11

RESULT 11
US-11-056-355B-106366
; Sequence 106366, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 106366
; LENGTH: 248
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 13619377
US-11-056-355B-106366
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Query Match 1.6%; Score 7; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 IDYIKYL 297
Db 20 IDYIKYL 26

RESULT 12

US-11-056-355B-117605
; Sequence 117605, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117605
; LENGTH: 248
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 13619377
US-11-056-355B-117605

Query Match 1.6%; Score 7; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 IDYIKYL 297
Db 20 IDYIKYL 26

RESULT 13

US-11-056-355B-106365
; Sequence 106365, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 106365
; LENGTH: 277
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13619376
US-11-056-355B-106365

Query Match 1.6%; Score 7; DB 7; Length 277;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 IDYIKYL 297

Db 49 IDYIKYL 55

RESULT 14

US-11-056-355B-117604
; Sequence 117604, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117604
; LENGTH: 277
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13619376
US-11-056-355B-117604

Query Match 1.6%; Score 7; DB 7; Length 277;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 IDYIKYL 297
Db 49 IDYIKYL 55

RESULT 15

US-10-953-349-27635
; Sequence 27635, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27635
; LENGTH: 293
; TYPE: prt
; ORGANISM: Triticum aestivum
US-10-953-349-27635

Query Match 1.6%; Score 7; DB 6; Length 293;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 SKSPPL 26
Db 205 SKSPPL 211

Search completed: August 11, 2006, 20:17:18
Job time : 17.9493 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2006, 19:53:30 ; Search time 116.721 Seconds
(without alignments)
1723.552 Million cell updates/sec

Title: US-10-764-212-18

Perfect score: 440

Sequence: 1 MFQPLLDATFESASIKRMPL.....YHKSILPLRAIRRWVKLGL 440

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	100.0	440	9	ABE70147 Helicobac
2	238	54.1	440	5	ABG30883
3	58	13.2	454	5	ABG30887
4	55	12.5	476	5	ABG30884
5	52	11.8	464	2	AAW86008
6	52	11.8	479	5	ABG30886
7	51	11.6	130	5	ABU51509
8	51	11.6	418	5	ABU52257
9	51	11.6	424	5	ABG30885
10	51	11.6	425	8	ADJ77820
11	51	11.6	425	8	ADJ27355
12	51	11.6	425	9	ABE70141
13	46	10.5	124	5	ABU51153
14	44	10.0	89	5	ABU51565
15	44	10.0	169	5	ABU51151
16	44	10.0	377	9	ABE70197
17	44	10.0	485	5	ABG30882
18	44	10.0	485	8	ADJ77814
19	44	10.0	485	8	ADJ27349
20	44	10.0	485	9	ABE70135
21	44	10.0	486	8	ADJ77810
22	44	10.0	486	8	ADJ27345
23	44	10.0	486	9	ABE70131

ALIGNMENTS

RESULT 1

ABE70147
ID ABE70147 standard; protein; 440 AA.

XX ABE70147;

XX AC ABE70147;

DT 06-OCT-2005 (first entry)

XX DE Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 18.

XX KW Fucosyltransferase; protein production; enzyme.

XX OS Helicobacter pylori; strain 802.

XX FH Key Location/Qualifiers

FT Misc-difference 112

XX /note= "Encoded by TTT"

XX PN US2005164338-A1.

XX PD 28-JUL-2005.

XX PF 22-JAN-2004; 2004US-00764212.

XX PR 22-JAN-2004; 2004US-00764212.

XX PA (NEOS-) NEOSE TECHNOLOGIES INC.

XX (UYAL-) UNIV ALBERTA.

XX PI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;

XX WPI; 2005-521417/53.

XX N-PSDB; ABE70146.

XX New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

XX Claim 1; SEQ ID NO 18; 97pp; English.

XX The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucose residue from a donor substrate and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

ABE70195 H. pylori
Adj77812 Helicobac
Adj27347 Alpha-1,3
ABE70133 Helicobac
ABE70204 H. pylori
ABE70149 Helicobac
ABE70205 H. pylori
ABE70199 H. pylori
Adj77816 Helicobac
Adj27351 Alpha-1,3
ABE70137 Helicobac
ABG30881 H. pylori
ABE70154 H. pylori
ABE70211 Helicobac
ABE70193 H. pylori
ABE70203 H. pylori
ABE70145 Helicobac
ABE70177 H. pylori
ABE70212 Helicobac
ABE70190 H. pylori
ABE70201 H. pylori

Db 421 YHKSPLLRATRRWVKGL 440
|||||

RESULT 3
ABG30887
ID ABG30887 standard; protein; 454 AA.

AC ABG30887;
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)

DE H. pylori alpha1,3 fucosyltransferase #7.

KW Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.

OS Helicobacter pylori; strain 11637.

PN US2002068347-A1.

PD 06-JUN-2002.

PF 07-DEC-2000; 2000US-00733524.

PR 05-JUN-1998; 98US-00092315.

PA (UYAL-) UNIV ALBERTA.

PI Taylor DE, Ge Z;

DR WPI; 2002-582480/62.

PT Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.

PS Example 3; Fig 6; 37pp; English.

CC The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpha1, 3- fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alpha1,3
CC fucosyltransferase encoded by the fucT gene. (Updated on 29-AUG-2003 to

CC standardise OS field)
XX
SQ Sequence 454 AA;

Query Match 13.2%; Score 58; DB 5; Length 454;
Best Local Similarity 100.0%; Pred. NO. 1e-48;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 EFLSQYKFNLCFNSQGYGVTEKIIDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDF 281
|||||
DB 227 EFLSQYKFNLCFNSQGYGVTEKIIDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDF 284
|||||

RESULT 4

ABG30884

ID ABG30884 standard; protein; 476 AA.

AC ABG30884;

DT 29-AUG-2003 (revised)

DT 21-OCT-2002 (first entry)

DE H. pylori alpha1,3 fucosyltransferase #4.

KW Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.

OS Helicobacter pylori; strain 26695A.

PN US2002068347-A1.

PD 06-JUN-2002.

PF 07-DEC-2000; 2000US-00733524.

PR 05-JUN-1998; 98US-00092315.

PA (UYAL-) UNIV ALBERTA.

PI Taylor DE, Ge Z;

DR WPI; 2002-582480/62.

PT Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.

PS Example 3; Fig 6; 37pp; English.

CC The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpha1, 3- fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the

CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alpha1,3
CC fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 476 AA;

Query Match 12.5%; Score 55; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-45; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKFTILENTIYHNPF 347
|||||
Db 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKFTILENTIYHNPF 351
|||||

RESULT 5
AAW86008
ID AAW86008 standard; protein; 464 AA.

XX AAW86008;

DT 17-OCT-2003 (revised)
DT 29-MAR-1999 (first entry)

XX Helicobacter pylori alpha-1,3-fucosyltransferase.

XX Alpha-1,3-fucosyltransferase; fuct gene; Lewis X; Lewis Y;
KW sialyl Lewis X; tumour associated antigen; cancer; infection;
XX mucosal disease; diagnosis; fucosylated oligosaccharide.

XX Helicobacter pylori; strain NCTC 11639.

XX Key Location/Qualifiers
FH Modified-site 96..99 /note= "Asn is N-glycosylated"
FT Modified-site 137..139 /note= "Asn is N-glycosylated"
FT Modified-site 332..334 /note= "Asn is N-glycosylated"
FT Modified-site 341..343 /note= "Asn is N-glycosylated"
FT Peptide 364..370 /note= "peptide repeat"
FT Peptide 371..377 /note= "peptide repeat"
FT Peptide 378..384 /note= "peptide repeat"
FT Peptide 385..391 /note= "peptide repeat"
FT Peptide 392..398 /note= "peptide repeat"
FT Peptide 399..405 /note= "peptide repeat"
FT Peptide 406..412 /note= "peptide repeat"
FT Peptide 413..419 /note= "peptide repeat"
FT Modified-site 435..437 /note= "Asn is N-glycosylated"

XX W09855630-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-CA000564.

PR 06-JUN-1997; 97US-0048857P.
XX (UYAL-) UNIV ALBERTA.

XX Taylor DE, Ge Z;

XX WPI; 1999-059913/05.

XX N-PSDB; AAV80321.

XX New isolated alpha-1,3-fucosyltransferase gene - obtained from
PT Helicobacter pylori, used to develop products for the diagnosis and
PT treatment of intestinal mucosal diseases, e.g. tumours.

XX Claim 6; Fig 2; 51pp; English.

XX This is the amino acid sequence of the novel alpha-1,3-
CC fucosyltransferase of Helicobacter pylori NCTC 11639, as deduced from the
CC newly isolated fuct gene (see AAV80321). The enzyme is characterised by 8
CC C-terminal heptad repeats and by the lack of a transmembrane domain. The
CC absence of a transmembrane domain allows the enzyme to be readily
CC released from recombinant host cells. The enzyme can be used in the
CC production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
CC sialyl Lewis X, which are structurally similar to certain tumour
CC associated antigens found in mammals. These glycoconjugates also have
CC research and diagnosis utility in the development of assays to detect
CC mammalian tumours. The enzyme can also be used to raise specific
CC antibodies. Inhibition of abnormal fuct gene product activity can be used
CC for the treatment of intestinal mucosal disease. (Updated on 17-OCT-2003
CC to standardise OS field)
XX

SQ Sequence 464 AA;

Query Match 11.8%; Score 52; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 1e-42; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 0;

Qy 239 QGYGVVTEKIIDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFKDFDAIDY 290
|||||
Db 242 QGYGVVTEKIIDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFKDFDAIDY 293
|||||

RESULT 6

ABG30886
ID ABG30886 standard; protein; 479 AA.

XX ABG30886;

XX 29-AUG-2003 (revised)

DT 21-OCT-2002 (first entry)

XX H. pylori alpha1,3 fucosyltransferase #6.

XX Enzyme; fuct; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.

XX Helicobacter pylori; strain 763.

XX US2002068347-A1.

XX 06-JUN-2002.

XX 07-DEC-2000; 2000US-00733524.

XX 05-JUN-1998; 98US-00092315.

XX (UYAL-) UNIV ALBERTA.

XX Taylor DE, Ge Z;

XX WPI; 2002-582480/62.

XX Purified transmembrane segment-free alpha1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.

XX Example 3; Fig 6; 37pp; English.

XX The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpha₁,3- fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpha₁,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha₁,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by *Helicobacter pylori* or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha₁,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha₁,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an *H. pylori* alpha₁,3
CC fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
CC standardise OS field)

XX Sequence 479 AA;

Query Match 11.8%; Score 52; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 QGYGVTEKIDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFKNFDAIDY 290
Db |||||
243 QGYGVTEKIDAYFSHTPIYWGSPSVAKDFNPKSFVNVDHFKNFDAIDY 294
|||||

RESULT 7
ABUS1509
ID ABUS1509 standard; protein; 130 AA.
XX
XX ABUS1509;
XX
DT 07-MAY-2003 (first entry)
DE *Helicobacter pylori* selected interacting domain (SID) protein #853.
KW Protein-protein interaction; ulcer; selected interacting domain; SID.
XX *Helicobacter pylori*.
OS
XX WO200266501-A2.
FN
XX 29-AUG-2002.
PD
XX 28-DEC-2001; 2001WO-EP015428.
PF
XX 02-JAN-2001; 2001US-0259302P.
PR
XX (HYBR-) HYBRIGENICS.
XX The invention describes a complex of protein-protein interactions in

PA (INSP) INST PASTEUR.
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
PI WPI; 2002-674910/72.
XX N-PSDB; ABX66254.
DR New complexes of protein-protein interactions in *Helicobacter pylori*,
DR useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals.
PT
XX Claim 6; Page 292; 642pp; English.
PS The invention describes a complex of protein-protein interactions in
XX *Helicobacter pylori* selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful for
CC screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This is the
CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an X to
CC represent an illegible residue
XX Sequence 130 AA;

Query Match 11.6%; Score 51; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 293 YLHTHPNAYLDMLYENPLNLDGKAYFYQDLGFKKILDPFKTILENDTIYH 343
Db |||||
2 YLHTHPNAYLDMLYENPLNLDGKAYFYQDLGFKKILDPFKTILENDTIYH 52
|||||

RESULT 8
ABUS2257
ID ABUS2257 standard; protein; 418 AA.
XX
XX ABUS2257;
XX
DT 07-MAY-2003 (first entry)
DE *Helicobacter pylori* selected interacting domain (SID) protein #1601.
XX Protein-protein interaction; ulcer; selected interacting domain; SID.
KW *Helicobacter pylori*.
OS
XX WO200266501-A2.
FN
XX 29-AUG-2002.
PD
XX 28-DEC-2001; 2001WO-EP015428.
PF
XX 02-JAN-2001; 2001US-0259302P.
PR
XX (HYBR-) HYBRIGENICS.
XX (INSP) INST PASTEUR.
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
PI WPI; 2002-674910/72.
XX N-PSDB; ABX67002.
DR New complexes of protein-protein interactions in *Helicobacter pylori*,
DR useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals.
PT
XX Claim 6; Page 479; 642pp; English.
PS The invention describes a complex of protein-protein interactions in

CC Helicobacter pylori selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful for
CC screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This is the
CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an X to
CC represent an illegible residue
XX
SQ Sequence 418 AA;

Query Match 11.6%; Score 51; DB 5; Length 418;
Best Local Similarity 100.0%; Pred. No. 9.3e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYH 343
|||||
DB 290 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYH 340
|||||

RESULT 9
ABG30885
ID ABG30885 standard; protein; 424 AA.

XX AC ABG30885;
XX
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)

XX DE H. pylori alpha1,3 fucosyltransferase #5.
XX
XX Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX
XX Helicobacter pylori; strain 26695B.
XX
XX US2002068347-A1.
XX
XX 06-JUN-2002.
XX
XX 07-DEC-2000; 2000US-00733524.
XX
XX 05-JUN-1998; 98US-00092315.
XX (UVAL-) UNIV ALBERTA.
XX
XX Taylor DE, Ge Z;
XX
XX WPI; 2002-582480/62.
XX
XX Purified transmembrane segment-free alpha1,3-fucosyltransferase
XX polypeptide useful for producing fucosylated oligosaccharides.
XX
XX Example 3; Fig 6; 37pp; English.

XX The invention relates a purified transmembrane segment-free alpha 1,3-
XX fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
XX Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
XX Ile, Val or Ala. Also included are the nucleic acid encoding the protein
XX (including its complement or fragment), a vector containing the nucleic
XX acid, a host cell containing nucleic acid or vector, an antibody which
XX selectively binds to the protein and a gene expression system for
XX producing transmembrane segment-free alpha1,3- fucosyltransferase,
XX comprising a host cell modified with the nucleic acid or its
XX enzymatically active portion. The protein and cells are useful for
XX producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
XX contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
XX and purifying the produced oligosaccharides, or by culturing the cell,
XX contacting the host cell with a substrate, to produce oligosaccharides
XX and purifying the obtained oligosaccharides. The nucleic acid is useful
XX as a probe for detecting the nucleic acid, by contacting a sample with a

CC nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alpha1,3
CC fucosyltransferase encoded by the fucT gene. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
SQ Sequence 424 AA;

Query Match 11.6%; Score 51; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.4e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYH 343
|||||
DB 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYH 347
|||||

RESULT 10
ADJ77820
ID ADJ77820 standard; protein; 425 AA.

XX AC ADJ77820;
XX
XX 06-MAY-2004 (first entry)
XX
XX Helicobacter pylori strain 26695 FucA protein SeqID 12.
XX
XX FucA; FucT; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX
XX Helicobacter pylori.
XX
XX WO2004009838-A2.
XX
XX 29-JAN-2004.
XX
XX 23-JUL-2003; 2003WO-US023057.
XX
XX 23-JUL-2002; 2002US-0398156P.
XX 08-NOV-2002; 2002US-0424894P.
XX
XX (NEOS-) NEOS TECHNOLOGIES INC.
XX
XX Johnson KP, Bezila DJ;
XX
XX WPI; 2004-123401/12.
XX N-PSDB; ADJ77819.
XX
XX New isolated polynucleotide encoding fucosyltransferase protein, useful
XX for synthesizing oligosaccharide moiety on a protein or lipid that is
XX unglycosylated in its native form or for synthesizing glycolipids.
XX
XX Claim 12; SEQ ID NO 12; 72pp; English.

XX This invention relates to novel isolated polynucleotides and the encoded
XX polypeptides thereof, which are related to the fucosyltransferase enzymes
XX (FucA and FucB) of Helicobacter pylori (H. pylori). Specifically, it
XX refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
XX chemically synthesise glycoproteins and glycolipids with the desired

CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of CC glycoconjugates. The present invention describes how bacterial CC fucosyltransferase is unaffected by the sialylation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, CC bacterially expressed enzymes offer a large cost saving relative to CC mammalian expression systems. This polypeptide sequence is an H. pylori CC strain 26695 Futa protein sequence of the invention.

XX
SQ Sequence 425 AA;

Query Match 11.6%; Score 51; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.5e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 343
DB 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 347

RESULT 11
ADJ27355
ID ADJ27355 standard; protein; 425 AA.

AC ADJ27355;
XX
XX 20-MAY-2004 (first entry)
XX
DE Alpha-1,3/4-fucosyltransferase.
XX
KW alpha-1,3/4-fucosyltransferase;
KW alpha-1,3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
XX fucosyl; fucose.

OS Helicobacter pylori; strain 26695Futa.

XX WO2004009793-A2.

XX 29-JAN-2004.

XX 23-JUL-2003; 2003WO-US023155.

XX 23-JUL-2002; 2002US-0398156P.

XX 08-NOV-2002; 2002US-0424894P.

XX (NEOS-) NBOSE TECHNOLOGIES INC.

XX Johnson KF, Bezila DJ;

XX WPI; 2004-132958/13.

XX N-PSDB; ADJ27354.

XX Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.

XX Example 1; Fig 6; 84pp; English.

XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.

XX Sequence 425 AA;

Query Match 11.6%; Score 51; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.5e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 343
DB 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 347

RESULT 12
AEB70141
ID AEB70141 standard; protein; 425 AA.

XX AEB70141;

XX 06-OCT-2005 (first entry)

XX Helicobacter pylori fucosyl transferase, Futa, protein, SEQ ID NO: 12.

XX Fucosyltransferase; protein production; enzyme.

XX Helicobacter pylori; strain 26695.

XX US2005164338-A1.

XX 28-JUL-2005.

XX 22-JAN-2004; 2004US-00764212.

XX 22-JAN-2004; 2004US-00764212.

XX (NEOS-) NBOSE TECHNOLOGIES INC.

XX (UYAL-) UNIV ALBERTA.

XX Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;

XX WPI; 2005-521417/53.

XX N-PSDB; AEB70140.

XX New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

XX Example 1; SEQ ID NO 12; 97pp; English.

XX The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The CC fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

XX Sequence 425 AA;

Query Match 11.6%; Score 51; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.5e-42;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 343
DB 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTIENDTIYH 347

RESULT 13
ABUS1153
ID ABUS1153 standard; protein; 124 AA.

XX AC ABUS1153;

XX 07-MAY-2003 (first entry)

XX Helicobacter pylori selected interacting domain (SID) protein #496.

XX Protein-protein interaction; ulcer; selected interacting domain; SID.

XX Helicobacter pylori.

CC amino acid sequence of a selected interacting domain (SID), identified
CC via protein-protein interactions. Note: Where the patent number printed
CC at the top of the pages in the specification has obscured areas of
CC protein sequence, the indexer has replaced the residue with an x to
CC represent an illegible residue

XX
SQ Sequence 169 AA;

Query Match 10.0%; Score 44; DB 5; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 MLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPF 347
DB 1 MLYENPLNTLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPF 44

Search completed: August 11, 2006, 20:00:03
Job time : 117.721 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:00:25 ; Search time 20.6557 Seconds
(without alignments)
2049.570 Million cell updates/sec

Title: US-10-764-212-18
Perfect score: 440
Sequence: 1 MFQPLLDAPFBSISIKMPL.....YHKSLPLLRARRWVKLGL 440

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	12.5	476	2 C64601	fucosyltransferase
2	51	11.6	425	2 C64567	fucosyltransferase
3	42	9.5	436	2 G71862	alpha-(1,3)-fucosyl
4	42	9.5	454	2 B71914	alpha-(1,3)-fucosyl
5	9	2.0	667	2 T09482	ring finger protein
6	8	1.8	287	2 A87080	probable regulator
7	8	1.8	354	2 S72958	hypothetical protein
8	8	1.8	392	2 F81676	heat shock gene re
9	8	1.8	656	2 T37941	conserved hypothet
10	8	1.8	745	2 B33856	hypothetical 80K p
11	8	1.8	1176	2 A33856	surface-layer 125K
12	8	1.8	1409	1 OFPFCP	copa polypeptide
13	8	1.8	3343	2 S44887	ZK12.7 protein -
14	7	1.6	128	2 AC0264	probable pyrophosph
15	7	1.6	152	2 C97249	probable nucleotid
16	7	1.6	153	2 B30131	hypothetical protein
17	7	1.6	162	2 H97620	hypothetical protein
18	7	1.6	162	2 AG2843	conserved hypothet
19	7	1.6	169	2 T26882	hypothetical protein
20	7	1.6	172	2 B71464	hypothetical protein
21	7	1.6	173	2 H84992	shikimate kinase (
22	7	1.6	173	2 AC1000	shikimate kinase (
23	7	1.6	173	2 AD0019	shikimate kinase (
24	7	1.6	174	2 G83712	hypothetical protein
25	7	1.6	177	2 C90170	hypothetical protein
26	7	1.6	184	2 E64443	hypothetical protein
27	7	1.6	215	2 A10696	probable type III
28	7	1.6	215	2 E84078	hypothetical protein
29	7	1.6	240	1 A65134	shikimate kinase (

30	7	1.6	240	2 H91157	shikimate kinase I
31	7	1.6	240	2 F86003	shikimate kinase I
32	7	1.6	252	2 S39556	lipoteichoic acid
33	7	1.6	267	2 T22978	hypothetical protein
34	7	1.6	279	2 B87434	hypothetical protein
35	7	1.6	279	2 G95545	hypothetical protein
36	7	1.6	298	2 S50964	hypothetical protein
37	7	1.6	312	2 H71876	glycerol-3-phosphat
38	7	1.6	312	2 A64640	glycerol-3-phosphat
39	7	1.6	321	2 F86864	homoserine O-succin
40	7	1.6	326	2 B75101	probable ATP-bindin
41	7	1.6	331	2 T41507	hypothetical protein
42	7	1.6	337	1 DESPGA	glycerol-3-phosphat
43	7	1.6	338	2 AG3582	iron(III)-binding
44	7	1.6	344	2 E84043	glycerol-3-phosphat
45	7	1.6	354	2 AC2601	hypothetical protein

ALIGNMENTS

RESULT 1

C64601 fucosyltransferase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64601

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalakh, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64601
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-476 <TOM>
A:Cross-references: UNIPROT:O25366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID:

Query Match 12.5%; Score 55; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e-48;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	293	YLHTPNAYLDMLYENPLNTLDGKAYFYQDLSPKKILDPEFKTILENDTIYHNNPF	347
DB	297	YLHTPNAYLDMLYENPLNTLDGKAYFYQDLSPKKILDPEFKTILENDTIYHNNPF	351

RESULT 2

C64567 fucosyltransferase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64567

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalakh, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64567
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <TOM>
A:Cross-references: UNIPROT:O25142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID:

Query Match 11.6%; Score 51; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	293	YLHTPNAYLDMLYENPLNTLDGKAYFYQDLSPKKILDPEFKTILENDTIYH	343
----	-----	---	-----

Db 297 YLHTHPNAYLDMYENPLNTLDGKAYFYQDLSPFKKILDFKTLLENTIYH 347
|||||
RESULT 3
G71862
alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <ARN>
A:Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI000000D36D2; GB:AE001439; NID
A:Experimental source: strain J99
Query Match 9.5%; Score 42; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.6e-35;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 280 DFKNFDEAIDVRYLHTHPNAYLDMYENPLNTLDGKAYFYQ 321
|||||
Db 283 DFKNFDEAIDVRYLHTHPNAYLDMYENPLNTLDGKAYFYQ 324
|||||
RESULT 4
B71914
alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: B71914
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <ARN>
A:Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI000000D3665; GB:AE001491; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: fuct
Query Match 9.5%; Score 42; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 6.6e-35;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 280 DFKNFDEAIDVRYLHTHPNAYLDMYENPLNTLDGKAYFYQ 321
|||||
Db 283 DFKNFDEAIDVRYLHTHPNAYLDMYENPLNTLDGKAYFYQ 324
|||||
RESULT 5
T09482
ring finger protein FXY - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
A:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of th
A:Reference number: Z16687
A:Accession: T09482

A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: UNIPROT:O15344; UNIPARC:UPI0000012F0E6; EMBL:AF035360; NID:G2827993; I
C:Genetics:
A:Gene: FXY
A:Map position: Xp22.3
C:Superfamily: rfp transforming protein
P:6-65/Domain: RING finger homology <RRN>
Query Match 2.0%; Score 9; DB 2; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 194 AFYDALNSI 202
|||||
Db 616 AFYDALNSI 624
|||||
RESULT 6
A87080
probable regulatory protein [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87080
R:Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: A87080
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-287 <STO>
A:Cross-references: UNIPROT:Q9CC29; UNIPARC:UPI000000C6D89; GB:AL450380; NID:G13093263; PJ
C:Genetics:
A:Gene: MLI367
C:Superfamily: regulatory protein spoJ
Query Match 1.8%; Score 8; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 355 EPLVSIDD 362
|||||
Db 97 EPLVSIDD 104
|||||
RESULT 7
S72958
hypothetical protein u0247b - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72958
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid L247.
A:Reference number: S72589
A:Accession: S72958
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <SMI>
A:Cross-references: UNIPROT:Q49889; UNIPARC:UPI000000B09BA; EMBL:U00021; NID:G467141; PID
C:Superfamily: regulatory protein spoJ
Query Match 1.8%; Score 8; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 355 EPLVSIDD 362
|||||

Db 164 EPLVSIDD 171

RESULT 8

P81676
heat shock gene repressor HcrA TC0673 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81676
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Grimm, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81676
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <TEXT>
A:CROSS-references: UNIPROT:P54306; UNIPARC:UPI00000579FA; GB:AE002336; GB:AE002160; NID:
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0673

Query Match 1.8%; Score 8; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 LVSIIDDLR 364

Db 153 LVSIIDDLR 160

RESULT 9

T37941
conserved hypothetical protein SPAC1952.13 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37941
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21755
A:Accession: T37941
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <MCD>
A:CROSS-references: UNIPROT:Q9UUJ6; UNIPARC:UPI000012FEP3; EMBL:AL109820; PIDN:CAB52577.
A:Experimental source: strain 972h; cosmid c1952
C:Genetics:
A:Gene: SPDB:SPAC1952.13
A:Map position: 1
A:Introns: 20/3; 114/3

Query Match 1.8%; Score 8; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 402 RSPILLELS 409

Db 580 RSPILLELS 587

RESULT 10

B33856
hypothetical 80K protein - Bacillus sphaericus
C:Species: Bacillus sphaericus
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993
C:Accession: B33856
R:Bowditch, R.D.; Baumann, P.; Yousten, A.A.
J. Bacteriol. 171, 4178-4188, 1989
A:Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer protein
A:Reference number: A33856; MUID:89327128; PMID:2666389
A:Accession: B33856
A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 1-745 <BOW>
A:CROSS-references: UNIPARC:UPI000017ACAS.

Query Match 1.8%; Score 8; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAYF 319

Db 16 TLDGKAYF 23

RESULT 11

A33856
surface-layer 125K protein precursor - Bacillus sphaericus
C:Species: Bacillus sphaericus
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33856
R:Bowditch, R.D.; Baumann, P.; Yousten, A.A.
J. Bacteriol. 171, 4178-4188, 1989
A:Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer protein
A:Reference number: A33856; MUID:89327128; PMID:2666389
A:Accession: A33856
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1176 <BOW>
A:CROSS-references: UNIPROT:P38537; UNIPARC:UPI000013SA02; GB:M28361; NID:G341911; PIDN:F;
F;93-147/Domain: S-layer repeat homology <SLR2>

Query Match 1.8%; Score 8; DB 2; Length 1176;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAYF 319

Db 398 TLDGKAYF 405

RESULT 12

OFFFCP
copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia
C:Contains: copia protein, 31k; copia protein, 48K; proteinase
C:Species: Drosophila melanogaster
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A03324; S03612; S14835
R:Mount, S.M.; Rubin, G.M.
Mol. Cell. Biol. 5, 1630-1638, 1985
A:Title: Complete nucleotide sequence of the Drosophila transposable element copia: homo
A:Reference number: A03324; MUID:85267679; PMID:2410772
A:Accession: A03324
A:Molecule type: DNA
A:Residues: 1-1409 <MOU>
A:CROSS-references: UNIPROT:P04146; UNIPARC:UPI0000127EE3; GB:M11240; NID:G158615; PIDN:
R:Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
Nucleic Acids Res. 17, 2134, 1989
A:Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A:Reference number: S03612; MUID:89183629; PMID:2538806
A:Accession: S03612
A:Molecule type: mRNA
A:Residues: 1-391,1375-1409 <MIL>
A:CROSS-references: UNIPARC:UPI000002A70E; EMBL:X13719; NID:G7745; PIDN:CAA31997.1; PID:
R:Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
EMBO J. 9, 535-541, 1990
A:Title: Virus-like particle formation of Drosophila copia through autocatalytic process
A:Reference number: S14835; MUID:90151630; PMID:1689241
A:Accession: S14835
A:Molecule type: DNA
A:Residues: 1-391,1375-1409 <YOS>
A:CROSS-references: UNIPARC:UPI000002A70E; EMBL:X54147; NID:G7749; PIDN:CAA38086.1; PID:
C:Genetics:
A:Gene: FlyBase:copia
A:CROSS-references: FlyBase:FBgn0000349

A:Mobile element: retrotransposon copia
C:Superfamily: retrovirus-related polyprotein
C:Keywords: polyprotein; proteinase
F;2-433/Product: copia protein, 48k #status predicted <MAT1>
F;2-270/Product: copia protein, 31k #status predicted <MAT2>
F;271-433/Product: proteinase #status predicted <MAT3>

Query Match 1.8%; Score 8; DB 1; Length 1409;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PPLKIAVA 30
Db 314 PPLKIAVA 321
|||||

RESULT 13

S44887
ZK112.7 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S44887

R;Du, Z.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK112.

A:Reference number: S44616

A:Accession: S44887

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-3343 <DUZ>

A:Cross-references: UNIPROT:P34616; UNIPARC:UPI000013BC7C; EMBL:L14324; NID:G289740; PID

C:Genetics:

A:Introns: 39/1; 74/3; 122/3; 209/2; 287/3; 333/2; 489/1; 611/2; 714/1; 939/3; 1002/2; 1

C:Keywords: cytoskeleton; transmembrane protein

Query Match 1.8%; Score 8; DB 2; Length 3343;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 ILENTIY 342
Db 2388 ILENTIY 2395
|||||

RESULT 14

AC0264

probable pyrophosphohydrolase nudG [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AC0264

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0264

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-128 <KUP>

A:Cross-references: UNIPROT:Q8ZEJ8; UNIPARC:UPI00000DCA34; GB:AL590842; PIDN:CAC90975.1;

C:Genetics:

A:Gene: nudG

C:Superfamily: mutator mutT; mutT domain homology

Query Match 1.6%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLLDAFI 10
Db 118 PLLDAFI 124
|||||

RESULT 15

C97249

probable nucleotide-binding protein, YjeE family [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C:Accession: C97249

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359125; PMID:21359325

A:Accession: C97249

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-152 <KUR>

A:Cross-references: UNIPROT:Q97FA2; UNIPARC:UPI00000CA45A; GB:AE001437; PIDN:AAK80782.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2838

C:Superfamily: ATPase likely involved in cell wall biosynthesis

Query Match 1.6%; Score 7; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 YAIGFDE 109
Db 87 YAIGFDE 93
|||||

Search completed: August 11, 2006, 20:09:15
Job time : 22.6557 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:54:19 ; Search time 155.082 Seconds
(without alignments)
2624.463 Million cell updates/sec

Title: US-10-764-212-18
Perfect score: 440
Sequence: 1 MFQPLLDAFIESIKMKPL.....YHKSLPLLAIRRWVKLGL 440

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	13.2	333	2	O32631_HELPHY
2	55	12.5	476	2	O25366_HELPHY
3	52	11.8	478	2	O30511_HELPHY
4	51	11.6	425	2	O25142_HELPHY
5	47	10.7	432	2	O68235_HELPHY
6	42	9.5	436	2	O92KD7_HELPHY
7	42	9.5	454	2	O32L13_HELPHY
8	32	7.3	462	2	O31884_HELPHY
9	9	2.0	94	2	O80Z72_MUSMA
10	9	2.0	94	2	O80Z75_MUSCE
11	9	2.0	94	2	O80Z78_MUSRI
12	9	2.0	94	2	O80Z81_ARVTE
13	9	2.0	94	2	O80Z85_MUSPL
14	9	2.0	94	2	O810Y0_MUSPI
15	9	2.0	108	1	TR118_MUSCR
16	9	2.0	667	1	TR118_HUMAN
17	9	2.0	667	1	TR118_MUSSP
18	9	2.0	667	1	TR118_RAT
19	8	1.8	96	2	O80410_CARPL
20	8	1.8	143	2	O8XSF7_DROME
21	8	1.8	153	2	O8SXG4_DROME
22	8	1.8	170	2	O89CB0_BRAJA
23	8	1.8	192	2	O3AS11_CHLCH
24	8	1.8	215	2	O32329_PSEPU
25	8	1.8	250	2	O798B1_MYCLE
26	8	1.8	273	2	O92XM4_9CAUD
27	8	1.8	287	2	O9CC29_MYCLE
28	8	1.8	297	2	O2S6L7_9SPHI
29	8	1.8	300	2	O8FU16_CORYB
30	8	1.8	320	2	O4BR25_BURVI
31	8	1.8	323	2	O7Q403_ANOHA

32	8	1.8	333	2	O8NZF1_STRP8
33	8	1.8	336	1	RUVB_HELHP
34	8	1.8	338	1	O2NIZ6_9MOLU
35	8	1.8	339	2	O3E2C5_BACTI
36	8	1.8	354	2	O49889_MYCLE
37	8	1.8	357	2	O8K5W1_STRP3
38	8	1.8	357	2	O99Y27_STRP1
39	8	1.8	359	2	O7VPA1_HELHP
40	8	1.8	380	2	O48RE1_STRPM
41	8	1.8	380	2	O48WN7_STRP1
42	8	1.8	380	2	O5XA00_STRP6
43	8	1.8	387	2	O4QKZ7_HAEI8
44	8	1.8	392	1	HRCA_CHLMU
45	8	1.8	395	2	O8TMT6_METAC

Q8nzf1	streptococc
Q7viu8	helicobacte
Q2niz6	aster yello
Q3ezc5	bacillus th
Q48899	mycobacteri
Q8k5w1	streptococc
Q99y27	streptococc
Q7vfa1	helicobacte
Q48re1	streptococc
Q48wn7	streptococc
Q5xa00	streptococc
Q4qkz7	haemophilus
P54306	chlamydia m
Q8tmt6	methanosaar

ALIGNMENTS

RESULT 1
O32631_HELPHY PRELIMINARY; PRT; 333 AA.
AC O32631; O32631; O32631;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-).
GN Name=fuct;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxId=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11637;
RX MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Bijnden D.H.,
RA Bird M.I.,
RT "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
alpha(1,3)-fucosyltransferase gene.";
RL J. Biol. Chem. 272:21349-21356(1997).
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EMBL; AF006039; AAB93985.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11929; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFCBIAAC127EOA8C CRC64;
Query Match 13.2%; Score 58; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.3e-51;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 EFLSYKKNLCPENSGQYGVTEKIIDAYFSHTIPYWGSPSVAKDFNPKSFVNVDHF 281
Db 106 EFLSYKKNLCPENSGQYGVTEKIIDAYFSHTIPYWGSPSVAKDFNPKSFVNVDHF 163
RESULT 2
O25366_HELPHY PRELIMINARY; PRT; 476 AA.
AC O25366;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Fucosyltransferase.
GN OrderedLocusNames=HP0651; ORFNames=HP_0651;

DR	GO; GO:0008417; F:fucoyltransferase activity; IEA.
DR	GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR	InterPro; IPR001503; Glyco trans 10.
DR	PANTHER; PTHR11929; Glyco trans 10; 1.
KW	Complete proteome; Glycosyltransferase; Transferase.
SQ	SEQUENCE 436 AA; 50699 MW; 1DB20666AE98FA61E CRC64;
Query Match 9.5%; Score 42; DB 2; Length 436;	
Best Local Similarity 100.0%; Pred. No. 3.6e-34;	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	280 DFKNFDPAIDYVRYLTHPNAYLDMLYENPLNTLDGKAYFYQ 321
DB	283 DFKNFDPAIDYVRYLTHPNAYLDMLYENPLNTLDGKAYFYQ 324
RESULT 7	
ID	Q9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
AC	Q9ZLI3;
DT	01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT	01-MAY-1999, sequence version 1.
DT	21-FEB-2006, entry version 23.
DE	ALPHA (1.3)-FUCOSYLTRANSFERASE.
GN	Name=fuct; ORFName=jhp_0596;
OS	Helicobacter pylori J99 (Campylobacter pylori J99).
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC	Helicobacteraceae; Helicobacter.
OX	NCBI_TaxID=85963;
RN	[1]
CC	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC	MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
CC	Alm R.A., Ling L.-S.L., Meir D.T., King B.L., Brown B.D., Doig P.C.,
CC	Smith D.B., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
CC	Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
CC	Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
CC	Trust T.J.;
CC	"Genomic sequence comparison of two unrelated isolates of the human
CC	gastric pathogen Helicobacter pylori.";
CC	Nature 397:176-180(1999).
CC	-----
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CC	-----
EMBL	AE001439; AAD06169.1; -; Genomic_DNA.
DR	PIR; B71914; B71914.
DR	BioCyc; HPYL85963:JHP0596-MONOMER; -.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0008417; F:fucoyltransferase activity; IEA.
DR	GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR	InterPro; IPR001503; Glyco trans 10.
DR	PANTHER; PTHR11929; Glyco trans 10; 1.
KW	Complete proteome; Glycosyltransferase; Transferase.
SQ	SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;
Query Match 9.5%; Score 42; DB 2; Length 454;	
Best Local Similarity 100.0%; Pred. No. 3.7e-34;	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	280 DFKNFDPAIDYVRYLTHPNAYLDMLYENPLNTLDGKAYFYQ 321
DB	283 DFKNFDPAIDYVRYLTHPNAYLDMLYENPLNTLDGKAYFYQ 324
RESULT 8	
Q9L8S4_HELPJ	
ID	Q9L8S4_HELPY PRELIMINARY; PRT; 462 AA.
AC	Q9L8S4;
DT	01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT	01-JUN-2003, sequence version 2.
DT	07-FEB-2006, entry version 17.

```
DE Alpha-1,3/4-fucosyltransferase.
GN Name=fucTa;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
RX Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RT "Cloning and characterization of the alpha(1,3/4) fucosyltransferase
of Helicobacter pylori.";
RL J. Biol. Chem. 275:4988-4994(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF194963; AA35291.2; -; Genomic_DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR INTERPRO; IPR001503; GlycoTrans10.
DR PANTHER; PTHR11929; GlycoTrans10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;

Query Match 7.3%; Score 32; DB 2; Length 462;
Best Local Similarity 100.0%; Pred.No. 9.6e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 DAYFSHTPIYWGSPSVAKDFNPKSFVNVDHP 281
Db 251 DAYFSHTPIYWGSPSVAKDFNPKSFVNVDHP 282

RESULT 9
Q80272 MUSMA
ID Q80272 MUSMA PRELIMINARY; PRT; 94 AA.
AC Q80272;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mus macedonicus (Macedonian mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=XBS;
RA MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RX Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
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CC -----
CC EMBL; AY181231; AA062991.1; -; Genomic_DNA.
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; Butyrophilin.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 11
Q80278 NMURI
ID Q80278 NMURI PRELIMINARY; PRT; 94 AA.
AC Q80278;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mastomys huberti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mastomys.
OX NCBI_TaxID=121569;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUBERTI;
RA MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RX Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
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CC -----
CC EMBL; AY181231; AA062991.1; -; Genomic_DNA.
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; Butyrophilin.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
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FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 10
Q80275 MUSCE
ID Q80275 MUSCE PRELIMINARY; PRT; 94 AA.
AC Q80275;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mus cervicolor (Fawn-colored mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CRIC;
RA MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RX Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
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CC -----
CC EMBL; AY181228; AA062988.1; -; Genomic_DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; Butyrophilin.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 11
Q80278 NMURI
ID Q80278 NMURI PRELIMINARY; PRT; 94 AA.
AC Q80278;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Fxy protein (Fragment).
GN Name=Fxy;
OS Mastomys huberti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mastomys.
OX NCBI_TaxID=121569;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUBERTI;
RA MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RX Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
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CC -----
CC EMBL; AY181228; AA062988.1; -; Genomic_DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; Butyrophilin.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;
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RX MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RA Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
CC -----
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CC -----
DR EMBL; AY181225; AAO62985.1; -; Genomic_DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003879; Butyrophylin.
DR InterPro; IPR003877; SPRY_rcpt.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1 94
FT SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 12
ID Q80281 ARVTE PRELIMINARY; PRT; 94 AA.
AC Q80281;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006; entry version 12.
DE Fxy protein (fragment).
GN Name=Fxy;
OS Arvicola terrestris (European water vole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Arvicolinae; Arvicola.
OX NCBI_TaxID=10050;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP InterPro; IPR001870; B302.
RP InterPro; IPR003879; Butyrophylin.
RP Pfam; PF00622; SPRY; 1.
RP PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1 94
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 13
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ID Q802B5_MUSPL PRELIMINARY; PRT; 94 AA.
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AC Q802B5;
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DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006; entry version 11.
DE Fxy (fragment).
OS Mus platythrix (Flat-haired mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10101;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PTX;
RP MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RA Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
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CC -----
DR EMBL; AY181234; AAO53222.1; -; Genomic_DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003879; Butyrophylin.
DR InterPro; IPR003877; SPRY_rcpt.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1 94
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Query Match 2.0%; Score 9; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 AFYDALNSI 202
Db 55 AFYDALNSI 63

RESULT 14
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ID Q810Y0 MUSSI PRELIMINARY; PRT; 94 AA.
AC Q810Y0;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006; entry version 12.
DE Fxy protein (fragment).
GN Name=Midl;
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ZRU;
RP MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
RA Montoya-Burgos J.I., Boursot P., Galtier N.;
RT "Recombination explains isochores in mammalian genomes.";
RL Trends Genet. 19:128-130(2003).
CC -----
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CC -----
DR EMBL; AY181237; AAO72140.1; -; Genomic_DNA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003879; Butyrophylin.
DR InterPro; IPR003877; SPRY_rcpt.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDUF.
FT NON_TER 1 94
FT SEQUENCE 94 AA; 10587 MW; 123565BBF9C7084F CRC64;
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Best Local Similarity 100.0%; Pred.No.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 AFYDALNSI 202
DB 55 AFYDALNSI 63

RESULT 15
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AC P82456;
DT 30-AUG-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2000, sequence version 1.
DT 07-MAR-2006, entry version 31.
DE Midline-1 (tripartite motif protein 18) (Fragment).
GN Name=Midi; Synonyms=Exy, Tri18;
OS Mus caroli (wild mouse) (Ricefield mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10089;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA]. DOI=10.1016/S0960-9822(99)80430-8;
RA MEDLINE=99439873; PubMed=10508587;
RA Perry J., Ashworth A.;
RT "Evolutionary rate of a gene affected by chromosomal position.";
RL Curr. Biol. 9:987-989(1999).
CC -!- FUNCTION: May have E3 ubiquitin ligase activity which targets the
CC catalytic subunit of protein phosphatase 2 for degradation (By
CC similarity).
CC -!- SUBUNIT: Homodimer or heterodimer with MID2. Interacts with IGBP1
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; microtubule-associated (By
CC similarity).
CC -!- SIMILARITY: Belongs to the TRIM/RBCC family.
CC -!- SIMILARITY: Contains 1 B30.2-like domain.
CC -----
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CC -----
DR EMBL; AF186462; AA01246.1; -; Genomic_DNA.
DR MGI; MGI:1100537; Midi.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003879; Butyrophilin.
DR InterPro; IPR003877; SPRY_rcpt.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF00622; SPRY; 1.
DR PRINTS; PR01407; BUTYPHLNCDF.
DR Ligase; Metal-binding; Microtubule; Phosphorylation;
KW Ubi conjugation pathway.
FT CHAIN <1 108 Midline-1.
FT DOMAIN <1 97 /FTID=PRO_0000056229.
FT NON_TER 1 1 B30.2-like.
SQ SEQUENCE 108 AA; 12195 MW; 8BDD3E2D9A8D61B5 CRC64;

Query Match 2.0%; Score 9; DB 1; Length 108;
Best Local Similarity 100.0%; Pred.No.2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 AFYDALNSI 202
DB 57 AFYDALNSI 65
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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:08:30 ; Search time 30.4918 Seconds
(without alignments)
1263.076 Million cell updates/sec

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Perfect score: 440
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649417

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	440	100.0	440	2	US-09-092-315-3
2	440	100.0	440	2	US-09-733-524A-3
3	440	100.0	440	2	US-10-189-977A-3
4	440	100.0	440	3	US-10-392-098A-3
5	58	13.2	454	2	US-09-092-315-8
6	58	13.2	454	2	US-09-733-524A-8
7	58	13.2	454	2	US-10-189-977A-8
8	58	13.2	454	3	US-10-392-098A-8
9	55	12.5	476	2	US-09-092-315-5
10	55	12.5	476	2	US-09-733-524A-5
11	55	12.5	476	2	US-10-189-977A-5
12	55	12.5	476	3	US-10-392-098A-5
13	52	11.8	372	2	US-09-092-315-13
14	52	11.8	464	2	US-09-092-315-1
15	52	11.8	464	2	US-09-733-524A-1
16	52	11.8	464	2	US-10-189-977A-1
17	52	11.8	464	3	US-10-392-098A-1
18	52	11.8	478	2	US-09-092-315-7
19	52	11.8	478	2	US-09-733-524A-7
20	52	11.8	478	2	US-10-189-977A-7
21	52	11.8	478	3	US-10-392-098A-7
22	51	11.6	425	2	US-09-092-315-6
23	51	11.6	425	2	US-09-733-524A-6
24	51	11.6	425	2	US-10-189-977A-6
25	51	11.6	425	3	US-10-392-098A-6
26	44	10.0	486	2	US-09-092-315-2

27	44	10.0	486	2	US-09-733-524A-2	Sequence 2, Appli
28	44	10.0	486	2	US-10-189-977A-2	Sequence 2, Appli
29	44	10.0	486	3	US-10-392-098A-2	Sequence 2, Appli
30	44	10.0	502	2	US-10-080-960-16	Sequence 16, Appl
31	9	2.0	415	2	US-09-949-016-11065	Sequence 11065, A
32	32	1.6	7	2	US-09-733-524A-26	Sequence 26, Appl
33	33	1.6	7	2	US-10-189-977A-26	Sequence 26, Appl
34	7	1.6	7	3	US-10-392-098A-26	Sequence 167, App
35	35	1.6	67	2	US-09-673-395A-167	Sequence 167, App
36	7	1.6	95	2	US-09-328-352-5647	Sequence 5647, Ap
37	7	1.6	109	2	US-09-270-767-44108	Sequence 44108, A
38	38	1.6	115	2	US-09-173-300-13	Sequence 13, Appl
39	39	1.6	115	2	US-10-027-450-13	Sequence 13, Appl
40	7	1.6	116	2	US-09-489-039A-13377	Sequence 13377, A
41	41	1.6	149	2	US-09-252-991A-28856	Sequence 28856, A
42	42	1.6	170	2	US-09-328-352-6822	Sequence 6822, Ap
43	43	1.6	181	2	US-09-270-767-45515	Sequence 45515, A
44	44	1.6	191	2	US-09-543-681A-6682	Sequence 6682, Ap
45	7	1.6	200	2	US-09-489-039A-10812	Sequence 10812, A

ALIGNMENTS

RESULT 1
US-09-092-315-3
; Sequence 3, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-3

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Qy	61	NEPSDLVFGSPITGAARKILSYQNTKRVFYAGENEVENFNFLFDYAIGFDELDRDYLRLMP	120		
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Qy	121	LYYDRLHKAESVNDTPAPYKIPDLSYTLKXPSHHFKRPHLCVAVNDESPLKRGFA	180		
Db	121	LYYDRLHKAESVNDTPAPYKIPDLSYTLKXPSHHFKRPHLCVAVNDESPLKRGFA	180		
Qy	181	SVFASNPAPKRNAPFDALNSIEPTVGGGSKNTLGKYGNKNEFLSOYKFNLCFENSQ	240		
Db	181	SVFASNPAPKRNAPFDALNSIEPTVGGGSKNTLGKYGNKNEFLSOYKFNLCFENSQ	240		
Qy	241	YGVVTEKILIDAFSHTIPIYWGSPSVAKDFNPKSFVNVDHFKNFDAIDVRYLHTHPNA	300		
Db	241	YGVVTEKILIDAFSHTIPIYWGSPSVAKDFNPKSFVNVDHFKNFDAIDVRYLHTHPNA	300		
Qy	301	YLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTLLENDTIYHNNPFVYFYRDLNEPLVSI	360		
Db	301	YLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTLLENDTIYHNNPFVYFYRDLNEPLVSI	360		

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US-10-189-977A-8

Query Match 13.2%; Score 58; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 EFLSQYKFNLCFNSQGYGVTEKIIDAYFSTHTPIYWGSPSVAKDFNPKSFVNVHDF 281
Db 227 EFLSQYKFNLCFNSQGYGVTEKIIDAYFSTHTPIYWGSPSVAKDFNPKSFVNVHDF 284

RESULT 8

US-10-392-098A-8
; Sequence 8, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; PRIOR FILING DATE: 2003-03-17
; PRIOR FILING DATE: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11637
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-8

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Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 227 EFLSQYKFNLCFNSQGYGVTEKIIDAYFSTHTPIYWGSPSVAKDFNPKSFVNVHDF 284

RESULT 9

US-09-092-315-5
; Sequence 5, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-5

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Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYHNNPF 351
RESULT 10
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
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; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match 12.5%; Score 55; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTLLENDTIYHNNPF 351

RESULT 11

US-10-189-977A-5
; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
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; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-5

Query Match 12.5%; Score 55; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 297 YLHTHPNAYLDMYENPLNTLGGKAYFYQDLSFKKILDPFKTILENDTIYHNPP 351
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RESULT 12
US-10-392-098A-5
; Sequence 5, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
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; PRIOR APPLICATION NUMBER: US 09/092,315
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; PRIOR APPLICATION NUMBER: US 09/733,524
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; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-5

Query Match 12.5%; Score 55; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 YLHTHPNAYLDMYENPLNTLGGKAYFYQDLSFKKILDPFKTILENDTIYHNPP 347
|||||
Db 297 YLHTHPNAYLDMYENPLNTLGGKAYFYQDLSFKKILDPFKTILENDTIYHNPP 351
|||||

RESULT 13
US-09-092-315-13
; Sequence 13, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-13

Query Match 11.8%; Score 52; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
|||||
Db 242 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 293
|||||

RESULT 14
US-09-092-315-1
; Sequence 1, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-1

Query Match 11.8%; Score 52; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
|||||
Db 242 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 293
|||||

RESULT 15
US-09-733-524A-1
; Sequence 1, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-1

Query Match 11.8%; Score 52; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
|||||
Db 242 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 293
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Job time : 31.4918 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2006, 20:09:35 ; Search time 106.23 Seconds
(without alignments)
1918.625 Million cell updates/sec

Title: US-10-764-212-18
Perfect score: 440
Sequence: 1 MFQPLLDAPFIESASIKKMP.....YHKSLPLLRATRWVKLGL 440

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	440	100.0	440	4	US-10-120-319-3
2	440	100.0	440	4	US-10-189-977-3
3	440	100.0	440	4	US-10-392-098-3
4	440	100.0	440	5	US-10-764-212-18
5	238	54.1	440	3	US-09-733-524-3
6	58	13.2	454	3	US-09-733-524-18
7	58	13.2	454	4	US-10-120-319-8
8	58	13.2	454	4	US-10-189-977-8
9	58	13.2	454	4	US-10-392-098-8
10	55	12.5	476	3	US-09-733-524-15
11	55	12.5	476	4	US-10-120-319-5
12	55	12.5	476	4	US-10-189-977-5
13	55	12.5	476	4	US-10-392-098-5
14	52	11.8	372	4	US-10-120-319-13
15	52	11.8	372	4	US-10-189-977-13
16	52	11.8	464	4	US-10-120-319-1
17	52	11.8	464	4	US-10-189-977-1
18	52	11.8	464	4	US-10-392-098-1
19	52	11.8	478	4	US-10-120-319-7
20	52	11.8	478	4	US-10-189-977-7
21	52	11.8	478	4	US-10-392-098-7
22	52	11.8	479	3	US-09-733-524-17
23	51	11.6	424	3	US-09-733-524-16
24	51	11.6	425	4	US-10-120-319-6
25	51	11.6	425	4	US-10-189-977-6
26	51	11.6	425	4	US-10-392-098-6
27	51	11.6	425	5	US-10-764-212-12

28	44	10.0	377	5	US-10-764-212-68	Sequence 68, Appl
29	44	10.0	485	3	US-09-733-524-2	Sequence 2, Appl
30	44	10.0	485	5	US-10-764-212-6	Sequence 6, Appl
31	44	10.0	486	4	US-10-120-319-2	Sequence 2, Appl
32	44	10.0	486	4	US-10-189-977-2	Sequence 2, Appl
33	44	10.0	486	4	US-10-392-098-2	Sequence 2, Appl
34	44	10.0	486	5	US-10-764-212-2	Sequence 2, Appl
35	44	10.0	502	3	US-09-844-948-5	Sequence 16, Appl
36	44	10.0	502	4	US-10-080-960-16	Sequence 16, Appl
37	44	10.0	502	4	US-10-184-648-23	Sequence 16, Appl
38	43	9.8	391	5	US-10-764-212-66	Sequence 66, Appl
39	43	9.8	432	5	US-10-764-212-4	Sequence 4, Appl
40	42	9.5	421	4	US-10-335-977-8558	Sequence 8558, Ap
41	42	9.5	436	4	US-10-335-977-8559	Sequence 8559, Ap
42	35	8.0	246	5	US-10-764-212-75	Sequence 75, Appl
43	32	7.3	456	5	US-10-764-212-20	Sequence 20, Appl
44	31	7.0	247	5	US-10-764-212-76	Sequence 76, Appl
45	31	7.0	256	5	US-10-764-212-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-10-120-319-3
; Sequence 3, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-3

Query Match	100.0%;	Score 440;	DB 4;	Length 440;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MFQPLLDAPFIESASIKKMP	LSYPPPLKIAVANWGGAEFFPKSAMYPILSQR	YITLHQN
QY	61	NEPSDLVFGSP	IGAAARKILSYQNTKVFYAGENEVFNFLFDYAIGFDELDRYL	RMP 120
Db	61	NEPSDLVFGSP	IGAAARKILSYQNTKVFYAGENEVFNFLFDYAIGFDELDRYL	RMP 120
QY	121	LYYDLRLHKAESVND	TTAPYKIPKPSLYTLKKPSHHFKKPHLCAVNDSDPLK	RGFA 180
Db	121	LYYDLRLHKAESVND	TTAPYKIPKPSLYTLKKPSHHFKKPHLCAVNDSDPLK	RGFA 180
QY	181	SVFASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEFLS	QYKFNLCFENS	Q 240
Db	181	SVFASNPAPKRNAPFYDALNSIEPVTGGSVKNTLGYKVGKNEFLS	QYKFNLCFENS	Q 240
QY	241	YGVTYKILIDAYFESH	TIPIYWGSPSAKDPNPKSFVNVDHDFKMFDEALDVRYL	LHHPNA 300
Db	241	YGVTYKILIDAYFESH	TIPIYWGSPSAKDPNPKSFVNVDHDFKMFDEALDVRYL	LHHPNA 300
QY	301	YLDMLYENPLNTLDGKAFYQDLSPFKKILDFFKTI	LENDTIYHNNPFVFFYRDLN	LEPLVSI 360
Db	301	YLDMLYENPLNTLDGKAFYQDLSPFKKILDFFKTI	LENDTIYHNNPFVFFYRDLN	LEPLVSI 360


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; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 802 FutA fucosyltransferase
US-10-764-212-18

Query Match      100.0%; Score 440; DB 5; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 MFQPLLDAPFTESASIKKMPISYPPPKIAVANWGWGAEPEKKSAMYPILSQRVTTITLHQP 60
Db    1 MFQPLLDAPFTESASIKKMPISYPPPKIAVANWGWGAEPEKKSAMYPILSQRVTTITLHQP 60

Qy    61 NEPSDLVFSGPIGAARKILSYONTKRVPFYAGENEVPNENFDYAIGFDELDLRDYLRLP 120
Db    61 NEPSDLVFSGPIGAARKILSYONTKRVPFYAGENEVPNENFDYAIGFDELDLRDYLRLP 120

Qy    121 LYDRLLHHKAESVNDDTTPAYKIKPDSLYTLKKPSHPHKPHLCVVNDSDPLKRGFA 180
Db    121 LYDRLLHHKAESVNDDTTPAYKIKPDSLYTLKKPSHPHKPHLCVVNDSDPLKRGFA 180

Qy    181 SFVASNPNAKRNAFYDALNISIEPVGTGGSVKNLTGYKVGNKNEFLSQYNLCFNFSOG 240
Db    181 SFVASNPNAKRNAFYDALNISIEPVGTGGSVKNLTGYKVGNKNEFLSQYNLCFNFSOG 240

Qy    241 YGVYTEKIIDAYSHTTIPIYWGSFSAVDNFKPNVVDKFNDPAEADYVRYLTHPNA 300
Db    241 YGVYTEKIIDAYSHTTIPIYWGSFSAVDNFKPNVVDKFNDPAEADYVRYLTHPNA 300

Qy    301 YLDMLYENPLNTLDGKAYFYQDSLFSFKILDFFKTILENDTIYHNPNPFVFRDLNEPLYSI 360
Db    301 YLDMLYENPLNTLDGKAYFYQDSLFSFKILDFFKTILENDTIYHNPNPFVFRDLNEPLYSI 360

Qy    361 DDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRSPLELSQNTTFKIYHKA 420
Db    361 DDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRSPLELSQNTTFKIYHKA 420

Qy    421 YHKSPLPLRAIRRWVKLG 440
Db    421 YHKSPLPLRAIRRWVKLG 440


RESULT 5
US-09-733-524-3
; Sequence 3, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 440
; TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 9.9e-47;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 281
Db 227 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284

RESULT 7

US-10-120-319-8
; Sequence 8, Application US/10120319
; Publication No. US2002016479A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-8

Query Match 13.2%; Score 58; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 9.9e-47;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

US-10-189-977-8
; Sequence 8, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-8

Query Match 13.2%; Score 58; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 9.9e-47;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 281
Db 227 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284

RESULT 9

US-10-392-098-8
; Sequence 8, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-8

Query Match 13.2%; Score 58; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 9.9e-47;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 281
Db 227 EFLSQKFNLCFENSQGGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284

RESULT 10

US-09-733-524-15
; Sequence 15, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695A
US-09-733-524-15

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Best Local Similarity 100.0%; Pred. No. 7.9e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 293 YLHTPHNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFKTLILENDTIYHNPF 347
Db

; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-13

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Best Local Similarity 100.0%; Pred. No. 4.9e-41;
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Qy 239 QGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDEAIDY 290
Db 242 QGYGVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVDKFNDEAIDY 293

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Job time : 107.23 secs

GenCore version 5.1.9
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Run on: August 11, 2006, 20:11:06 ; Search time 16.7213 Seconds
(without alignments)
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Title: US-10-764-212-18

Perfect score: 440

Sequence: 1 MFQPLDLAFIESASIKRMPL.....YHKSLPLRAIRRWVKLGL 440

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Gapop 60.0 , Gapext 60.0

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Word size : 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.0	667	7 US-11-289-102-250	Sequence 250, App
2	7	1.6	238	6 US-10-449-902-31893	Sequence 31893, A
3	7	1.6	238	6 US-10-449-902-47233	Sequence 47233, A
4	7	1.6	259	6 US-10-953-349-26636	Sequence 26636, A
5	7	1.6	259	7 US-11-056-355B-67711	Sequence 67711, A
6	7	1.6	270	7 US-11-056-355B-15997	Sequence 15997, A
7	7	1.6	276	6 US-10-953-349-26635	Sequence 26635, A
8	7	1.6	276	7 US-11-056-355B-67710	Sequence 67710, A
9	7	1.6	326	6 US-10-449-902-46731	Sequence 46731, A
10	7	1.6	334	7 US-11-056-355B-15996	Sequence 15996, A
11	7	1.6	339	7 US-11-056-355B-100768	Sequence 100768, A
12	7	1.6	339	7 US-11-056-355B-112007	Sequence 112007, A
13	7	1.6	357	7 US-11-056-355B-15995	Sequence 15995, A
14	7	1.6	358	7 US-11-056-355B-100767	Sequence 100767, A
15	7	1.6	358	7 US-11-056-355B-112006	Sequence 112006, A
16	7	1.6	363	7 US-11-056-355B-63558	Sequence 63558, A
17	7	1.6	365	7 US-11-056-355B-63557	Sequence 63557, A
18	7	1.6	373	7 US-11-056-355B-100766	Sequence 100766, A
19	7	1.6	373	7 US-11-056-355B-112005	Sequence 112005, A
20	7	1.6	398	7 US-11-056-355B-63556	Sequence 63556, A
21	7	1.6	405	6 US-10-953-349-3312	Sequence 3312, Ap
22	7	1.6	415	6 US-10-449-902-37072	Sequence 37072, A
23	7	1.6	452	7 US-11-056-355B-58710	Sequence 58710, A
24	7	1.6	462	7 US-11-056-355B-58709	Sequence 58709, A
25	7	1.6	469	6 US-10-953-349-3311	Sequence 3311, Ap

Sequence 8574, Ap
Sequence 17428, A
Sequence 8573, Ap
Sequence 17427, A
Sequence 12, Appl
Sequence 3310, Ap
Sequence 58708, A
Sequence 8572, Ap
Sequence 17426, A
Sequence 31462, A
Sequence 6280, A
Sequence 31461, A
Sequence 6279, A
Sequence 31247, A
Sequence 50578, A
Sequence 31460, A
Sequence 6278, A
Sequence 6, Appl
Sequence 4, Appl
Sequence 54865, A

7 US-11-056-355B-8574
7 US-11-056-355B-17428
7 US-11-056-355B-8573
7 US-11-056-355B-17427
7 US-11-275-569-12
6 US-10-953-349-3310
7 US-11-056-355B-58708
7 US-11-056-355B-8572
7 US-11-056-355B-17426
6 US-10-953-349-31462
7 US-11-056-355B-6280
6 US-10-953-349-31461
7 US-11-056-355B-6279
6 US-10-449-902-31247
6 US-10-449-902-50578
6 US-10-953-349-31460
7 US-11-056-355B-6278
6 US-10-519-335-6
6 US-10-519-335-4
6 US-10-449-902-54865

ALIGNMENTS

RESULT 1

US-11-289-102-250
; Sequence 250, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-250

Query Match 2.0%; Score 9; DB 7; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 194 AFYDALNSI 202
|||
Db 616 AFYDALNSI 624

RESULT 2

US-10-449-902-31893
; Sequence 31893, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31893
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31893

Query Match 1.6%; Score 7; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 DLNEPLV 358
| | | | |
Db 9 DLNEPLV 15

RESULT 3

US-10-449-902-47233
; Sequence 47233, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47233
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47233

Query Match 1.6%; Score 7; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 DLNEPLV 358
| | | | |
Db 9 DLNEPLV 15

RESULT 4

US-10-953-349-26636
; Sequence 26636, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26636
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26636

Query Match 1.6%; Score 7; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 57;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 424 SLPLLR 430
| | | | |
Db 14 SLPLLR 20

RESULT 5

US-11-056-355B-67711
; Sequence 67711, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67711
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(259)
; OTHER INFORMATION: Ceres Seq. ID no. 13595883
US-11-056-355B-67711

Query Match 1.6%; Score 7; DB 7; Length 259;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 SLPLLR 430
| | | | |
Db 14 SLPLLR 20

RESULT 6

US-11-056-355B-15997
; Sequence 15997, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 15997
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(270)
; OTHER INFORMATION: Ceres Seq. ID no. 12407516
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (237)..(237)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-056-355B-15997

Query Match 1.6%; Score 7; DB 7; Length 270;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; APPLICANT: National Institute of Agrobiological Sciences
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46731
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46731

Query Match      1.6%; Score 7; DB 6; Length 326;
Best Local Similarity 100.0%; Pred.No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      418 HKAYHKS 424
Db      94 HKAYHKS 100
      |||||

RESULT 10
US-11-056-355B-15996
; Sequence 15996, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119965
; SEQ ID NO 15996
; LENGTH: 334
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres Seq. ID no. 12407515
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (301)..(301)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-056-355B-15996

Query Match      1.6%; Score 7; DB 7; Length 334;
Best Local Similarity 100.0%; Pred.No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      312 TLDGKAY 318
Db      113 TLDGKAY 119
      |||||

RESULT 11
US-11-056-355B-100768
; Sequence 100768, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav

```


; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 100768
; LENGTH: 339
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(339)
; OTHER INFORMATION: Ceres Seq. ID no. 13606035
US-11-056-355B-100768

Query Match 1.6%; Score 7; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAY 318
| | | | |
Db 327 TLDGKAY 333

RESULT 12
US-11-056-355B-112007
; Sequence 112007, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112007
; LENGTH: 339
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(339)
; OTHER INFORMATION: Ceres Seq. ID no. 13606035
US-11-056-355B-112007

Query Match 1.6%; Score 7; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAY 318
| | | | |
Db 327 TLDGKAY 333

RESULT 13
US-11-056-355B-15995
; Sequence 15995, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B

; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 15995
; LENGTH: 357
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(357)
; OTHER INFORMATION: Ceres Seq. ID no. 12407514
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-056-355B-15995

Query Match 1.6%; Score 7; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAY 318
| | | | |
Db 136 TLDGKAY 142

RESULT 14
US-11-056-355B-100767
; Sequence 100767, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 100767
; LENGTH: 358
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(358)
; OTHER INFORMATION: Ceres Seq. ID no. 13606034
US-11-056-355B-100767

Query Match 1.6%; Score 7; DB 7; Length 358;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLDGKAY 318
| | | | |
Db 346 TLDGKAY 352

RESULT 15
US-11-056-355B-112006
; Sequence 112006, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 112006
; LENGTH: 358
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(358)
; OTHER INFORMATION: Ceres Seq. ID no. 13606034
US-11-056-3558-112006

Query Match 1.6%; Score 7; DB 7; Length 358;
Best Local Similarity 100.0%; Pred.No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 TLGKAY 318
|||
Db 346 TLGKAY 352

Search completed: August 11, 2006, 20:17:17
Job time : 17.7213 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	456	100	0	456	9	AE870149	Helicobac
2	201	44	1	227	9	AE870154	H. pylori
3	201	44	1	559	9	AE870211	Helicobac
4	68	14	9	418	5	ABU52257	Helicobac
5	68	14	9	424	5	AC830885	H. pylori
6	68	14	9	425	8	ADJ77820	Helicobac
7	68	14	9	425	8	ADJ27355	Alpha-1,3
8	68	14	9	425	9	AE870141	Helicobac
9	68	14	9	476	5	AC830884	H. pylori
10	50	11	0	446	9	AE870145	Helicobac
11	46	10	1	391	9	AE870195	H. pylori
12	46	10	1	432	8	ADJ77812	Helicobac
13	46	10	1	432	8	ADJ27347	Alpha-1,3
14	46	10	1	432	9	AE870133	Helicobac
15	41	9	0	454	5	AC830887	H. pylori
16	39	8	6	49	5	AC832639	Helicobac
17	39	8	6	169	5	ABU51151	Helicobac
18	39	8	6	171	9	AE870190	H. pylori
19	39	8	6	485	5	AC830882	H. pylori
20	39	8	6	485	8	ADJ77814	Helicobac
21	39	8	6	485	8	ADJ27349	Alpha-1,3
22	39	8	6	485	9	AE870135	Helicobac
23	39	8	6	486	8	ADJ77810	Helicobac

Best Local Similarity 100.0%; Pred. No. 0;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQPLDADFIDSTHLDTHKPLNVALANWPLKSEKKGFRDPILHPILKQRYKIILH 60
Db 1 MFQPLDADFIDSTHLDTHKPLNVALANWPLKSEKKGFRDPILHPILKQRYKIILH 60

Qy 61 SNNEPSDLVFGNPLEQARKILSYQNTKRVFTYTGNEVPNPNFLDYAIGFDELDFNDRL 120
Db 61 SNNEPSDLVFGNPLEQARKILSYQNTKRVFTYTGNEVPNPNFLDYAIGFDELDFNDRL 120

Qy 121 RMPLYAYLHYKAMLVNDTTSYKALYTLKPKSHKFKENHPNLCALIHNESDPWKRGF 180
Db 121 RMPLYAYLHYKAMLVNDTTSYKALYTLKPKSHKFKENHPNLCALIHNESDPWKRGF 180

Qy 181 ASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNKNEFLSQYKFNLCFENSQ 240
Db 181 ASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNKNEFLSQYKFNLCFENSQ 240

Qy 241 GYGVTTEKILDAYFESHPIYWGSPSVAKDPNPKSFVNVDHFNPNFDEAIDYIRYLHAHQN 300
Db 241 GYGVTTEKILDAYFESHPIYWGSPSVAKDPNPKSFVNVDHFNPNFDEAIDYIRYLHAHQN 300

Qy 301 AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNILENDTIYHCNDARYSALHRDLNEP 360
Db 301 AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFKNILENDTIYHCNDARYSALHRDLNEP 360

Qy 361 LVSVDLRRDHDRLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLRRDHDRLRDH 420
Db 361 LVSVDLRRDHDRLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLRRDHDRLRDH 420

Qy 421 ERLLSKATPILLESQNTSFKIYKAYOKSLPILRAI 456
Db 421 ERLLSKATPILLESQNTSFKIYKAYOKSLPILRAI 456

RESULT 2
AEB70154
ID AEB70154 standard; protein; 227 AA.
XX AEB70154;
XX
DT 06-OCT-2005 (first entry)
XX
DE H. pylori fucosyl transferase, FutA, protein fragment, SEQ ID NO: 25.
XX
KW Fucosyltransferase; protein production.
XX
OS Helicobacter pylori; strain 955.
XX
PN US2005164338-A1.
XX
PD 28-JUL-2005..
XX
PF 22-JAN-2004; 2004US-00764212.
XX
PR 22-JAN-2004; 2004US-00764212.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
PA (UVAL-) UNIV ALBERTA.
XX
PI Simala-Grant J, Taylor D, Johnson KF, Bezila DV;
XX WPI; 2005-521417/53.
XX
PT New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
PS Disclosure; SEQ ID NO 25; 97pp; English.
XX
CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a

CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein fragment.
XX
SQ Sequence 227 AA;

Query Match 44.1%; Score 201; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-195; Indels 0; Gaps 0;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 FILKQRYKIILHSPNEPSDLVFGNPLEQARKILSYQNTKRVFTYTGNEVPNPNFLDYAI 108
Db 26 FILKQRYKIILHSPNEPSDLVFGNPLEQARKILSYQNTKRVFTYTGNEVPNPNFLDYAI 85

Qy 109 GFDELDFNDRLRVNPLYYAYLHYKAMLVNDTTSYKALYTLKPKSHKFKENHPNLCAL 168
Db 86 GFDELDFNDRLRVNPLYYAYLHYKAMLVNDTTSYKALYTLKPKSHKFKENHPNLCAL 145

Qy 169 IHNESDPWKRGFASVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNKNEFLS 228
Db 146 IHNESDPWKRGFASVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNKNEFLS 205

Qy 229 QYKFNLCFENSQGYGVTEKI 249
Db 206 QYKFNLCFENSQGYGVTEKI 226

RESULT 3
AEB70211
ID AEB70211 standard; protein; 559 AA.
XX AEB70211;
AC AEB70211;
XX
DT 06-OCT-2005 (first entry)
XX
DE Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 22 #2.
XX
KW Fucosyltransferase; protein production; enzyme.
XX
OS Helicobacter pylori; strain 955.
XX
FH Key Location/Qualifiers
FT Misc-difference 38 /note= "Encoded by TAA"
FT Misc-difference 50 /note= "Encoded by TAA"
FT Misc-difference 57 /note= "Encoded by TAG"
FT Misc-difference 61 /note= "Encoded by TAG"
FT Misc-difference 72 /note= "Encoded by TAA"
FT Misc-difference 300 /note= "Encoded by TGA"
FT Misc-difference 321 /note= "Encoded by TAA"
FT Misc-difference 323 /note= "Encoded by TAA"
FT Misc-difference 330 /note= "Encoded by TGA"
FT Misc-difference 335.336 /note= "Encoded by TGATGA"
FT Misc-difference 339 /note= "Encoded by TGA"
FT Misc-difference 357 /note= "Encoded by TGA"
FT Misc-difference 364 /note= "Encoded by TGA"
FT Misc-difference 376 /note= "Encoded by TGA"
FT Misc-difference 387 /note= "Encoded by TGA"

FT Misc-difference 396 /note= "Encoded by TGA"
FT Misc-difference 405 /note= "Encoded by TGA"
FT Misc-difference 408 /note= "Encoded by TGA"
FT Misc-difference 414. .415 /note= "Encoded by TGA"
FT Misc-difference 421. .422 /note= "Encoded by TGA"
FT Misc-difference 426 /note= "Encoded by TGA"
FT Misc-difference 428. .429 /note= "Encoded by TGA"
FT Misc-difference 435 /note= "Encoded by TGA"
FT Misc-difference 454 /note= "Encoded by TGA"
FT Misc-difference 475 /note= "Encoded by TAA"
FT Misc-difference 475 /note= "Encoded by TAA"
FT Misc-difference 495 /note= "Encoded by TAA"
FT Misc-difference 509 /note= "Encoded by TAA"
FT Misc-difference 514 /note= "Encoded by TAA"
FT Misc-difference 520 /note= "Encoded by TAA"
FT Misc-difference 534 /note= "Encoded by TAA"
FT Misc-difference 549 /note= "Encoded by TGA"
FT Misc-difference 554 /note= "Encoded by TAA"
XX /note= "Encoded by TAA"

US2005164338-A1.

28-JUL-2005.

22-JAN-2004; 2004US-00764212.

22-JAN-2004; 2004US-00764212.

(NEOS-) NEOSE TECHNOLOGIES INC.
(UTAL-) UNIV ALBERTA.

Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;

WPI; 2005-521417/53.
N-PSDB; ABB70150.

New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

Example 4; SEQ ID NO 22; 97pp; English.

The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein. Note: The present sequence is the SEQ ID NO: 22 which is shown in the example 4 (figure 21) of the specification. This sequence differs from the SEQ ID NO: 22 given in the sequence listing.

Sequence 559 AA;

Query Match 44.1%; Score 201; DB 9; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 FILKORYKIILHSNPNEPSDLVFGNPLEQARKILSYQNTXRVFYTGNEVPNLFDAI 108
DB FILKORYKIILHSNPNEPSDLVFGNPLEQARKILSYQNTXRVFYTGNEVPNLFDAI 157
QY 109 GFDELDPNDRYLRLMPLYAYLHYKAMLVNDTTSFYKLYTLLKPSHKFKNHPNLCA 168
DB 158 GFDELDPNDRYLRLMPLYAYLHYKAMLVNDTTSFYKLYTLLKPSHKFKNHPNLCA 217
QY 169 IHNESDPWKGFGFASVFNAPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNNEPLS 228
DB 218 IHNESDPWKGFGFASVFNAPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKKNNEPLS 277
QY 229 QYKFNLCFENSQGYGVVTEKI 249
DB 278 QYKFNLCFENSQGYGVVTEKI 298

RESULT 4

ABU52257

ID ABU52257 standard; protein; 418 AA.

AC ABU52257;

XX 07-MAY-2003 (first entry)

DE Helicobacter pylori selected interacting domain (SID) protein #1601.

KW Protein-protein interaction; ulcer; selected interacting domain; SID.

OS Helicobacter pylori.

PN WO200266501-A2.

PD 29-AUG-2002.

XX 28-DEC-2001; 2001WO-EP015428.

XX 02-JAN-2001; 2001US-0259302P.

XX (HYBR-) HYBRIGENICS.

PA (INSP) INST PASTEUR.

XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;

DR WPI; 2002-674910/72.

DR N-PSDB; ABX67002.

XX New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.

PS Claim 6; Page 479; 642pp; English.

XX The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. CC Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the CC amino acid sequence of a selected interacting domain (SID), identified CC via protein-protein interactions. Note: Where the patent number printed CC at the top of the pages in the specification has obscured areas of CC protein sequence, the indexer has replaced the residue with an X to CC represent an illegible residue

XX Sequence 418 AA;

Query Match 14.9%; Score 68; DB 5; Length 418;

Best Local Similarity 100.0%; Pred. No. 7.8e-60;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 RFLSYKFNLCFENSQGYGVVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284

Db 221 EFLSQYKFNLCFENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 280
QY 285 FDEAIDYI 292
Db 281 FDEAIDYI 288
RESULT 5
ABG30885
ID ABG30885 standard; protein; 424 AA.
XX
XX ABG30885;
XX AC
XX 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
XX H. pylori alphas, 3 fucosyltransferase #5.
XX
XX Enzyme; fucT; alphas, 3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX
XX Helicobacter pylori; strain 26695B.
XX OS
XX US2002068347-A1.
XX PN
XX 06-JUN-2002.
XX PD
XX 07-DEC-2000; 2000US-00733524.
XX PF
XX 05-JUN-1998; 98US-00092315.
XX PR
XX (UYAL-) UNIV ALBERTA.
XX PA
XX Taylor DE, Ge Z;
XX PI
XX WPI; 2002-582480/62.
XX DR
XX
XX Purified transmembrane segment-free alphas, 3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.
XX PT
XX Example 3; Fig 6; 37pp; English.
XX PS
XX
XX The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alphas, 3-fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacMac-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alphas, 3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alphas, 3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alphas, 3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alphas, 3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using

CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alphas, 3
CC fucosyltransferase encoded by the fucT gene. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 424 AA;
Query Match 14.9%; Score 68; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 7.9e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 EFLSQYKFNLCFENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295
RESULT 6
ADJ77820
ID ADJ77820 standard; protein; 425 AA.
XX AC
XX ADJ77820;
XX DT
XX 06-MAY-2004 (first entry)
XX DE
XX Helicobacter pylori strain 26695 FucA protein SeqID 12.
XX KW
XX FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
XX fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX OS
XX Helicobacter pylori.
XX WO2004009838-A2.
XX PN
XX 29-JAN-2004.
XX PD
XX 23-JUL-2003; 2003WO-US023057.
XX PF
XX 23-JUL-2002; 2002US-0398156P.
XX PR 08-NOV-2002; 2002US-0424894P.
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI Johnson KF, Bezila DJ;
XX DR WPI; 2004-123401/12.
XX DR N-PSDB; ADJ77819.
XX
XX New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
PT unglycosylated in its native form or for synthesizing glycolipids.
XX
XX Claim 12; SEQ ID NO 12; 72pp; English.
XX
XX This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesise glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar, as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 26695 FucA protein sequence of the invention.
XX
SQ Sequence 425 AA;

```
Query Match      14.9%; Score 68; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 8e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
DB 228 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
DB 288 FDEAIDYI 295

RESULT 7
ADJ27355
ID ADJ27355 standard; protein; 425 AA.
XX AC
XX ADJ27355;
XX AC
XX 20-MAY-2004 (first entry)
XX DT
XX DE Alpha-1,3/4-fucosyltransferase.
XX KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
XX KW fucosyl; fucose.
XX OS Helicobacter pylori; strain 26695FutA.
XX PI
XX PN WO2004009793-A2.
XX PD
XX 29-JAN-2004.
XX PF
XX 23-JUL-2003; 2003WO-US023155.
XX PR
XX 23-JUL-2002; 2002US-0398156P.
XX PR 08-NOV-2002; 2002US-0424894P.
XX XX
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI
XX Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX DR N-PSDB; ADJ27354.
XX XX
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX PS
XX Example 1; Fig 6; 84pp; English.
XX CC
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated
CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.
XX XX
XX Sequence 425 AA;

Query Match      14.9%; Score 68; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 8e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
DB 228 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
DB 288 FDEAIDYI 295

RESULT 8
AEB70141
ID AEB70141 standard; protein; 425 AA.
XX XX
XX AC AEB70141;
XX XX
XX 06-OCT-2005 (first entry)
XX DT
XX DE Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 12.
XX KW
XX Fucosyltransferase; protein production; enzyme.
XX OS
XX Helicobacter pylori; strain 26695.
XX PN US2005164338-A1.
XX PD
XX 28-JUL-2005.
XX PF
XX 22-JAN-2004; 2004US-00764212.
XX PR
XX 22-JAN-2004; 2004US-00764212.
XX XX
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PA (UYAL-) UNIV ALBERTA.
XX XX
XX Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX PI
XX WPI; 2005-521417/53.
XX DR N-PSDB; AEB70140.
XX XX
XX New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX PS
XX Example 1; SEQ ID NO 12; 97pp; English.
XX CC
XX The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.
XX XX
XX Sequence 425 AA;

Query Match      14.9%; Score 68; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 8e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
DB 228 EFLSQYKFLNCFENSGQGYVTEKILDYFSTHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
DB 288 FDEAIDYI 295

RESULT 9
ABG30884
ID ABG30884 standard; protein; 476 AA.
XX XX
XX AC ABG30884;
XX XX
XX 29-AUG-2003 (revised)
XX DT 21-OCT-2002 (first entry)
XX XX
XX H. pylori alpha1,3 fucosyltransferase #4.
XX KW
XX Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
XX sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
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XX OS Helicobacter pylori; strain 26695A.
XX PN US2002068347-A1.
XX PD 06-JUN-2002.
XX PF 07-DEC-2000; 2000US-00733524.
XX PR 05-JUN-1998; 98US-00092315.
XX PA (UYAL-) UNIV ALBERTA.
XX PI Taylor DE, Ge Z;
XX PD WPI; 2002-582480/62.
XX PF Purified transmembrane segment-free alphas 1,3-fucosyltransferase
PT polypeptide useful for producing fucosylated oligosaccharides.
XX PS Example 3; Fig 6; 37pp; English.
XX CC The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X1-X2-
CC Leu-Arg-X3-X4-Tyr, where X1, X2 and X4 is Asp or Asn; and X3 is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpha 1,3-fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpha 1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha 1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha 1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha 1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. pylori alpha 1,3
CC fucosyltransferase encoded by the fucT gene. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX SQ Sequence 476 AA;
Query Match 14.9%; Score 68; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.8e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 EFLSQKFNLCFNSQGYGVTEKILDYFHSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
DB 228 EFLSQKFNLCFNSQGYGVTEKILDYFHSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
DB 288 FDEAIDYI 295

RESULT 10
AEB70145
ID AEB70145 standard; protein; 446 AA.
XX AC AEB70145;
XX DT 06-OCT-2005 (first entry)
XX DE Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 16.
XX KW Fucosyltransferase; protein production; enzyme.
XX OS Helicobacter pylori; strain 1111.
XX FH Key Location/Qualifiers
FT Misc-difference 168 /note= "Encoded by GC"
FT Misc-difference 355 /note= "Encoded by AG"
FT Misc-difference 408 /note= "Encoded by AG"
FT Misc-difference 435 /note= "Encoded by AG"
XX PN US2005164338-A1.
XX PD 28-JUL-2005.
XX PF 22-JAN-2004; 2004US-00764212.
XX PR 22-JAN-2004; 2004US-00764212.
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI (UYAL-) UNIV ALBERTA.
XX SI Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
XX N-PSDB; AEB70144.
XX CC New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX PS Claim 1; SEQ ID NO 16; 97pp; English.
XX CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.
XX SQ Sequence 446 AA;
Query Match 11.0%; Score 50; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 EFLSQKFNLCFNSQGYGVTEKILDYFHSHTPIYWGSPSVAKDFNPK 274
DB 227 EFLSQKFNLCFNSQGYGVTEKILDYFHSHTPIYWGSPSVAKDFNPK 276
RESULT 11
AEB70195
ID AEB70195 standard; protein; 391 AA.
XX AC AEB70195;
XX DT 06-OCT-2005 (first entry)
XX DE H. pylori fucosyl transferase, FutA, protein fragment, SEQ ID NO: 66.

XX Fucosyltransferase; protein production; enzyme.
KW Helicobacter pylori; strain 1111.
OS US2005164338-A1.
FN 28-JUL-2005.
XX 22-JAN-2004; 2004US-00764212.
XX 22-JAN-2004; 2004US-00764212.
FR (NEOS-) NEOF TECHNOLOGIES INC.
XX (UVAL-) UNIV ALBERTA.
PA Sinala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
XX New isolated fucosyltransferase polynucleotides and polypeptides, useful
PT for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX Disclosure; SEQ ID NO 66; 97pp; English.
XX The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase catalytic domain
CC (amino acids 27-417) protein fragment.
XX Sequence 391 AA;
SQ Query Match 10.1%; Score 46; DB 9; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNDFNDFEADIDYIRYLH 296
Db 226 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNDFNDFEADIDYIRYLH 271
RESULT 12
ADJ77812
ID ADJ77812 standard; protein; 432 AA.
XX AC ADJ77812;
XX 06-MAY-2004 (first entry)
XX Helicobacter pylori strain 1111 Futa protein SeqID 4.
DE Futa; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
XX fucose; N-acetylglucosamine; glycoconjugate; enzyme.
KW Helicobacter pylori.
XX OS WO2004009838-A2.
XX PN 29-JAN-2004.
XX 23-JUL-2003; 2003WO-US023057.
XX 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX (NEOS-) NEOF TECHNOLOGIES INC.
XX Johnson KF, Bezila DJ;
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which

DR WPI; 2004-123401/12.
XX N-PSDB; ADJ77811.
XX New isolated polynucleotide encoding fucosyltransferase protein, useful
PT for synthesizing oligosaccharide moiety on a protein or lipid that is
PT unglycosylated in its native form or for synthesizing glycolipids.
XX Claim 16; SEQ ID NO 4; 72pp; English.
XX This invention relates to novel isolated polynucleotides and the encoded
CC polypeptides thereof, which are related to the fucosyltransferase enzymes
CC (Futa and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC chemically synthesize glycoproteins and glycolipids with the desired
CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC acetylglucosamine), such that they are useful in the preparation of
CC glycoconjugates. The present invention describes how bacterial
CC fucosyltransferase is unaffected by the sialylation status of the acceptor
CC sugar, as opposed to the mammalian homologue, and furthermore,
CC bacterially expressed enzymes offer a large cost saving relative to
CC mammalian expression systems. This polypeptide sequence is an H. pylori
CC strain 1111 Futa protein sequence of the invention.
XX Sequence 432 AA;
SQ Query Match 10.1%; Score 46; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNDFNDFEADIDYIRYLH 296
Db 252 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHFNDFNDFEADIDYIRYLH 297
RESULT 13
ADJ27347
ID ADJ27347 standard; protein; 432 AA.
XX AC ADJ27347;
XX 20-MAY-2004 (first entry)
XX Alpha-1,3/4-fucosyltransferase.
DE alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
XX fucose.
KW Helicobacter pylori; strain 1111 PutA.
XX OS WO2004009793-A2.
XX PN 29-JAN-2004.
XX 23-JUL-2003; 2003WO-US023155.
XX 23-JUL-2002; 2002US-0398156P.
PR 08-NOV-2002; 2002US-0424894P.
XX (NEOS-) NEOF TECHNOLOGIES INC.
XX Johnson KF, Bezila DJ;
XX WPI; 2004-132958/13.
XX N-PSDB; ADJ27346.
XX Producing fucosylated glycoprotein, by contacting recombinant
PT fucosyltransferase protein with mixture comprising donor substrate and
PT acceptor substrate on glycoprotein.
XX Claim 1; Fig 2; 84pp; English.
XX This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC was used in the method of the invention for producing a fucosylated

CC glycoprotein. The method involves contacting a recombinant
CC fucosyltransferase protein with a mixture comprising a donor substrate
CC which comprises a fucosyl residue, and an acceptor substrate on a
CC glycoprotein, under conditions such that the fucosyltransferase protein
CC catalyzes the transfer of the fucose residue from a donor substrate to
CC the acceptor substrate on the glycoprotein. The method is useful for
CC producing fucosylated glycoprotein.

XX
XX
SQ Sequence 432 AA;

Query Match 10.1%; Score 46; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DAYFSTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
DB 252 DAYFSTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 297
|||||

RESULT 14

ABE70133

ID ABE70133 standard; protein; 432 AA.

XX
XX AC ABE70133;
XX
DT 06-OCT-2005 (first entry)
XX
DB Helicobacter pylori fucosyl transferase, PutA, protein, SEQ ID NO: 4.
XX
XX Fucosyltransferase; protein production; enzyme.
XX
XX Helicobacter pylori; strain 1111.
XX
XX US2005164338-A1.
XX
XX 28-JUL-2005.
XX
XX 22-JAN-2004; 2004US-00764212.
XX
XX 22-JAN-2004; 2004US-00764212.
XX
XX (NEOS-) NEOSR TECHNOLOGIES INC.
XX (UVAL-) UNIV ALBERTA.
XX
XX Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
XX WPI; 2005-521417/53.
XX N-PSDB; ABE70132.
XX
XX New isolated fucosyltransferase polynucleotides and polypeptides, useful
XX for synthesizing oligosaccharides, glycoproteins, or glycolipids.
XX
XX Example 1; SEQ ID NO 4; 97pp; English.

CC The present invention provides alpha-1,3/4-fucosyltransferase (also
CC termed as fucosyltransferase) proteins and nucleic acids from various
CC strains of Helicobacter pylori. This enzyme catalyzes the transfer of a
CC fucose residue from a donor substrate to an acceptor substrate. The
CC fucosyltransferase polynucleotides and polypeptides are useful for the
CC synthesis of oligosaccharides, glycoproteins and glycolipids. The present
CC sequence is Helicobacter pylori fucosyltransferase protein.

XX
XX
SQ Sequence 432 AA;

Query Match 10.1%; Score 46; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DAYFSTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
DB 252 DAYFSTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 297
|||||

RESULT 15

ABG30887

ID ABG30887 standard; protein; 454 AA.

XX
XX AC ABG30887;
XX
DT 29-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
XX H. pylori alpha1,3 fucosyltransferase #7.
XX
XX Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
KW slxex; Helicobacter pylori infection; malignant cell; mammalian tumour.
XX
XX Helicobacter pylori; strain 11637.
XX
XX US2002068347-A1.
XX
XX 06-JUN-2002.
XX
XX 07-DEC-2000; 2000US-00733524.
XX
XX 05-JUN-1998; 98US-00092315.
XX (UVAL-) UNIV ALBERTA.
XX
XX Taylor DE, Ge Z;
XX WPI; 2002-582480/62.
XX
XX Purified transmembrane segment-free alpha1,3-fucosyltransferase
XX polypeptide useful for producing fucosylated oligosaccharides.
XX
XX Example 3; Fig 6; 37pp; English.

CC The invention relates a purified transmembrane segment-free alpha 1,3-
CC fucosyltransferase polypeptide, having a repeat of the sequence: X₁-X₂-
CC Leu-Arg-X₃-X₄-Tyr, where X₁, X₂ and X₄ is Asp or Asn; and X₃ is
CC Ile, Val or Ala. Also included are the nucleic acid encoding the protein
CC (including its complement or fragment), a vector containing the nucleic
CC acid, a host cell containing nucleic acid or vector, an antibody which
CC selectively binds to the protein and a gene expression system for
CC producing transmembrane segment-free alpha1,3- fucosyltransferase,
CC comprising a host cell modified with the nucleic acid or its
CC enzymatically active portion. The protein and cells are useful for
CC producing fucosylated oligosaccharides, such as Lex, Ley or slxex, by
CC contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
CC and purifying the produced oligosaccharides, or by culturing the cell,
CC contacting the host cell with a substrate, to produce oligosaccharides
CC and purifying the obtained oligosaccharides. The nucleic acid is useful
CC as a probe for detecting the nucleic acid, by contacting a sample with a
CC nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
CC polynucleotide, and detecting hybridisation of the probe; or by
CC amplifying the nucleic acid using polymerase chain reaction (PCR). The
CC host cell is useful for producing a transmembrane segment-free alpha1,3-
CC fucosyltransferase-fusion protein, by growing the host cell containing a
CC vector operably linked to a polynucleotide encoding a desired polypeptide
CC or peptide under conditions which allow expression and secretion of the
CC fusion protein and isolating the fusion protein. The antibody is useful
CC for detecting the protein in a sample. The presence of the protein in the
CC sample is indicative of infection by Helicobacter pylori or the presence
CC of malignant cells. The antibody is also useful for diagnosing disorders
CC and monitoring disease, and for inhibiting abnormal alpha1,3-
CC fucosyltransferase gene product activity. The nucleic acid is useful as
CC part of ribozyme and/or triple helix sequences and for alpha1,3-
CC fucosyltransferase gene regulation. Oligosaccharides synthesised using
CC the protein or cell are useful in the development of assays to detect
CC mammalian tumours. The present sequence represents an H. Pylori alpha1,3
CC fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
CC standardise OS field)

XX
XX Sequence 454 AA;

	Query Match	9.0%	Score 41;	DB 5;	Length 454;
	Best Local Similarity	100.0%;	Pred. No. 2.2e-32;		
	Matches 41;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	251	DAYFSHTIIYWGSPSVAKDFNPKGSFVNVDHFNNFDEADY	291		
Db	253	DAYFSHTIIYWGSPSVAKDFNPKGSFVNVDHFNNFDEADY	293		

Search completed: August 11, 2006, 20:00:02
Job time : 121.966 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:00:25 ; Search time 21.4069 Seconds
(without alignments)
2049.570 Million cell updates/sec

Title: US-10-764-212-20

Perfect score: 456

Sequence: 1 MFQPLLDADFIDSTHLDETH.....TSFKYKAYOKSLPLRAI 456

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	14.9	425	2 C64567	fucosyltransferase
2	68	14.9	476	2 C64601	fucosyltransferase
3	39	8.6	454	2 B71914	alpha (1,3)-fucosyl
4	38	8.3	436	2 G71862	alpha-(1,3)-fucosyl
5	8	1.8	174	2 G83712	hypothetical prote
6	8	1.8	289	2 S39814	DNA polymerase hom
7	8	1.8	764	1 H70414	conserved hypothet
8	8	1.8	3343	2 S44887	ZK112.7 protein -
9	7	1.5	79	2 T10336	hypothetical prote
10	7	1.5	89	2 A43854	major merozoite su
11	7	1.5	128	2 AC0264	probable pyrophosp
12	7	1.5	128	2 P75276	large conductance
13	7	1.5	138	2 P00125	major merozoite su
14	7	1.5	146	2 S03290	Glycoprotein, 190K
15	7	1.5	152	2 C97249	probable nucleotid
16	7	1.5	153	2 B90131	hypothetical prote
17	7	1.5	154	2 B82457	hypothetical prote
18	7	1.5	162	2 H97620	hypothetical prote
19	7	1.5	162	2 AG2843	conserved hypothet
20	7	1.5	197	2 G64329	anthranilate synth
21	7	1.5	208	2 B75359	endopeptidase-rela
22	7	1.5	215	2 B84078	hypothetical prote
23	7	1.5	216	2 T22314	hypothetical prote
24	7	1.5	218	2 T47706	hypothetical prote
25	7	1.5	228	2 C69859	two-component resp
26	7	1.5	233	2 B24796	glycerolaldehyde-3-p
27	7	1.5	232	2 AD25814	glycoprotein 185 -
28	7	1.5	305	1 S52775	hypothetical prote
29	7	1.5	310	2 D70818	hypothetical prote

30	7	1.5	312	2 H71876	glycerol-3-phospha
31	7	1.5	312	2 A64640	glycerol-3-phospha
32	7	1.5	314	2 D87576	oxidoreductase, al
33	7	1.5	336	2 A24430	glycerolaldehyde-3-p
34	7	1.5	338	2 AG3582	iron(III)-binding
35	7	1.5	354	2 AC3601	hypothetical prote
36	7	1.5	357	2 T23311	hypothetical prote
37	7	1.5	359	1 DEUT1C	glycerolaldehyde-3-p
38	7	1.5	364	2 D97383	hypothetical prote
39	7	1.5	385	2 B24430	glycerolaldehyde-3-p
40	7	1.5	392	2 T32555	hypothetical prote
41	7	1.5	396	2 JQ1285	glycerolaldehyde-3-p
42	7	1.5	399	2 F86262	Flk33.15 protein
43	7	1.5	401	2 B84060	multidrug resistanc
44	7	1.5	405	1 DEPMNA	glycerolaldehyde-3-p
45	7	1.5	417	2 C44038	tryptophan permeas

ALIGNMENTS

RESULT 1

C64567 fucosyltransferase - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: C64567

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: C64567

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-425 <TOM>

A:Cross-references: UNIPROT:O25142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID:

Query Match 14.9%; Score 68; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. NO. 1.4e-63;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	225	EFLSQKYNLCFNSQGYVTEKILDAYFSHTPIYWGSPSVAKDPNPKSFVNVDHFN	284
DB	228	EFLSQKYNLCFNSQGYVTEKILDAYFSHTPIYWGSPSVAKDPNPKSFVNVDHFN	287
QY	285	FDEAIDYI 292	
DB	288	FDEAIDYI 295	

RESULT 2

C64601 fucosyltransferase - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: C64601

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: C64601

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-476 <TOM>

A:Cross-references: UNIPROT:O25366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID:

Query Match 14.9%; Score 68; DB 2; Length 476;

```
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83712
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <STO>
A;Cross-references: UNIPROT:Q9KPH6; UNIPARC:UPI00000C38D5; GB:AP001508; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0503
C;Superfamily: Deinococcus radiodurans hypothetical protein DR0763

Query Match      1.8%; Score 8; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      299 QNAYLDML 306
Db      14 QNAYLDML 21

RESULT 6
S39814
DNA polymerase homolog pol-r - rye mitochondrion (strain Halo)
C;Species: mitochondrion Secale cereale (rye)
A;Variety: strain Halo
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S39814
R;Dohmen, G.; Tudzynski, P.
Curr. Genet. 25, 59-65, 1994
A;Title: A DNA-polymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.
A;Reference number: S39814; MUID:94363738; PMID:8082167
A;Accession: S39814
A;Molecule type: DNA
A;Residues: 1-289 <DOH>
A;Cross-references: UNIPROT:Q36545; UNIPARC:UPI000008F158; EMBL:X74132; NID:9439279; PID:
A;Experimental source: strain Halo; etiolated shoots
C;Genetics:
A;Gene: pol-r
A;Genome: mitochondrion
C;Keywords: mitochondrion

Query Match      1.8%; Score 8; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      9 FIDSTHLD 16
Db      20 FIDSTHLD 27

RESULT 7
H70414
conserved hypothetical protein aq_1328 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H70414
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70414
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-764 <AQF>
A;Cross-references: UNIPROT:O67347; UNIPARC:UPI00000565BC; GB:AE000734; GB:AE000657; NID:
A;Experimental source: strain VFS
```

```
Best Local Similarity 100.0%; Pred. No. 1.6e-63;
Matches      68; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      225 EFLSQYKFNLCFNSQGYGVTEKILDAYSHTPIYWGSPSVAKDNPKSFVNVDHFN 284
Db      228 EFLSQYKFNLCFNSQGYGVTEKILDAYSHTPIYWGSPSVAKDNPKSFVNVDHFN 287

Qy      285 FDEAIDYI 292
Db      288 FDEAIDYI 295

RESULT 3
B71914
alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <ARN>
A;Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: fucT

Query Match      8.6%; Score 39; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 8.9e-33;
Matches      39; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      372 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 410
Db      364 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 402

RESULT 4
G71862
alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <ARN>
A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000D36D2; GB:AE001528; GB:AE001439; NID
A;Experimental source: strain J99

Query Match      8.3%; Score 38; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.8e-32;
Matches      38; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      78 ARKILSYQNTKRVFTGENEVPNENFLDYAIGFDELDF 115
Db      78 ARKILSYQNTKRVFTGENEVPNENFLDYAIGFDELDF 115

RESULT 5
G83712
hypothetical protein BH0503 [imported] - Bacillus halodurans (strain C-125)
```

C:Genetics:

A:Gene: aq_1328
C:Superfamily: Aquifex aeolicus conserved hypothetical protein aq_1328
C:Keywords: ATP, nucleotide binding, P-loop
F:70-77/Region: nucleotide-binding motif A (P-loop)
F:162-165/Region: DEXH motif

Query Match 1.8%; Score 8; DB 1; Length 764;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 ALYTLKPK 154
|||
Db 254 ALYTLKPK 261

RESULT 8

S44887
ZK112.7 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S44887
R:Du, Z.

A:Submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK112.
A:Reference number: S44616

A:Accession: S44887
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3343 <DUZ>
A:Cross-references: UNIPROT:P34616; UNIPARC:UPI000013BC7C; EMBL:L14324; NID:g289740; P1

C:Genetics:
A:Introns: 39/1; 74/3; 122/3; 209/2; 287/3; 333/2; 489/1; 611/2; 714/1; 939/3; 1002/2; 1
C:Keywords: cytoskeleton; transmembrane protein

Query Match 1.8%; Score 8; DB 2; Length 3343;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 ILENDTIY 343
|||
Db 2388 ILENDTIY 2395

RESULT 9

Ti0336
hypothetical protein 67 - Orgyia pseudotsugata nuclear polyhedrosis virus

C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpNPV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: Ti0336

R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997

A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: Ti0336

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-79 <AHR>
A:Cross-references: UNIPROT:O10321; UNIPARC:UPI000006182F; EMBL:U75930; NID:g2934903; P1

Query Match 1.5%; Score 7; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 EKILDAY 253
|||
Db 9 EKILDAY 15

RESULT 10

A43854
major merozoite surface protein gp195 - malaria parasite (Plasmodium falciparum) (fragme
C:Species: Plasmodium falciparum

C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004

C:Accession: A43854
R:Hui, G.S.; Hashimoto, A.; Chang, S.P.

Infect. Immun. 60, 1422-1433, 1992
A:Title: Roles of conserved and allelic regions of the major merozoite surface protein (g
A:Reference number: A43854; MUID:92192814; PMID:1548068
A:Accession: A43854

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <HUI>
A:Cross-references: UNIPROT:Q8T6A9; UNIPARC:UPI0000177F83
A:Experimental source: FVO isolate
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:89242, NCBIP:89243)

Query Match 1.5%; Score 7; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 VASGGSV 212
|||
Db 60 VASGGSV 66

RESULT 11

AC0264
Probable pyrophosphohydrolase nudG [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC0264
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0264
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-128 <KUR>
A:Cross-references: UNIPROT:Q8ZEU8; UNIPARC:UPI00000DCA34; GB:AL590842; PIDN:CAC90975.1;

C:Genetics:
A:Gene: nudG
C:Superfamily: mutator mutT; mutT domain homology

Query Match 1.5%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLLDAFI 10
|||
Db 118 PLLDAFI 124

RESULT 12

F75276
large conductance mechanosensitive channel - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: F75276

R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75276

A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-128 <WHI>
A:Cross-references: UNIPROT:Q9RRR4; UNIPARC:UPI00000D3FB5; GB:AE002072; GB:AE000513; NID:

A:Experimental source: strain R1
C:Genetics:

A;Gene: DR2422
A;Map position: 1
C;Superfamily: yhcD protein

Query Match 1.5%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GFRDFIL 47
| | | | |
Db 4 GFRDFIL 10

RESULT 13

PQ0125
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (isolate B439
N;Alternate names: gp195, PMSA, PSA

C;Species: Plasmodium falciparum
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 31-Dec-2004

C;Accession: PQ0125

R;Kimura, E.; Mattei, D.; di Santi, S.M.; Scherf, A.

Gene 91, 57-62, 1990

A;Title: Genetic diversity in the major merozoite surface antigen of Plasmodium falciparum
A;Reference number: PQ0120; MUID:90382698; PMID:2205540

A;Accession: PQ0125

A;Molecule type: DNA

A;Residues: 1-138 <KIM>

A;Cross-references: UNIPROT:Q25960; UNIPARC:UPI0000082067; GB:M32116; NID:g160502; PIDN:
C;Superfamily: G surface protein

C;Keywords: glycoprotein; surface antigen

Query Match 1.5%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 VASGGSV 212
| | | | |
Db 44 VASGGSV 50

RESULT 14

S03290
glycoprotein, 190K - malaria parasite (Plasmodium falciparum) (isolate Bandia-Senegal)

C;Species: Plasmodium falciparum

A;Variety: isolate Bandia-Senegal

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C;Accession: S03290

R;Scherf, A.; Barbot, P.; Langale, G.

Nucleic Acids Res. 17, 1774, 1989

A;Title: Sequence and length polymorphism of a major malaria vaccine candidate analysed
A;Reference number: S03290; MUID:89160345; PMID:2646601

A;Accession: S03290

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-146 <SCH>

A;Cross-references: UNIPROT:Q8TG69; UNIPROT:Q9TZV2; UNIPROT:Q9TZU9; UNIPARC:UPI0000177F8
C;Keywords: glycoprotein

Query Match 1.5%; Score 7; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 VASGGSV 212
| | | | |
Db 64 VASGGSV 70

RESULT 15

C97249
probable nucleotide-binding protein, YjeE family [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C;Accession: C97249

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359125; PMID:21359325

A;Accession: C97249

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-152 <KUR>

A;Cross-references: UNIPROT:Q97PA2; UNIPARC:UPI00000CA65A; GB:AE001437; PIDN:AAK80782.1;
A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC2838

C;Superfamily: ATPase likely involved in cell wall biosynthesis

Query Match 1.5%; Score 7; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 YAIGFDE 112
| | | | |
Db 87 YAIGFDE 93

Search completed: August 11, 2006, 20:09:13

Job time : 25.4069 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 11, 2006, 19:54:19 ; Search time 160.721 Seconds
(without alignments)
2624.463 Million cell updates/sec

Title: US-10-764-212-20
Perfect score: 456
Sequence: 1 MFQPLDAFIDSTHLDTH.....TSFKIYRKAYQKSLPLRAI 456

Scoring table: 'OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	100.0	462	2	Q9L8S4_HELPPY
2	71	15.6	432	2	Q6ST35_HELPPY
3	68	14.9	425	2	Q25142_HELPPY
4	68	14.9	476	2	Q25366_HELPPY
5	41	9.0	333	2	Q32631_HELPPY
6	39	8.6	454	2	Q92L31_HELPPY
7	38	8.3	436	2	Q92KD7_HELPPY
8	32	7.0	478	2	Q30511_HELPPY
9	9	2.0	308	2	Q9FDN3_BACFR
10	9	2.0	308	2	Q5LFQ8_BACFR
11	9	2.0	308	2	Q9FDN4_BACFR
12	8	1.8	151	2	Q8FR14_COREF
13	8	1.8	154	2	Q34YL2_GAMMM
14	8	1.8	159	2	Q8XY28_RALSO
15	8	1.8	170	2	Q48279_HAESO
16	8	1.8	170	2	Q89CH0_BRAJA
17	8	1.8	174	2	Q9KHF6_BACHD
18	8	1.8	192	2	Q3AS11_CHLCH
19	8	1.8	202	2	Q33G46_METHU
20	8	1.8	204	2	Q4HJ36_CAMLA
21	8	1.8	215	2	Q92329_PSEPU
22	8	1.8	263	2	Q6ZFQ3_ORYSA
23	8	1.8	267	2	Q5CHD4_CRYHO
24	8	1.8	267	2	Q7YVL3_CRYPV
25	8	1.8	289	2	Q36545_SECC
26	8	1.8	303	2	Q368C1_GAMMM
27	8	1.8	323	2	Q7Q403_ANOGA
28	8	1.8	338	2	Q2NI26_WMOLU
29	8	1.8	359	2	Q7VPA1_HELHP
30	8	1.8	361	2	Q4AS02_BURK
31	8	1.8	364	2	Q44EK1_CHRSL

32	8	1.8	395	2	Q8TWT6_METAC	Q8Tmt6 methanosarc
33	8	1.8	398	2	Q4JVZ8_CORJK	Q4jvz8 corynebacte
34	8	1.8	401	1	ASSY CORGL	Q85176 corynebacte
35	8	1.8	421	2	Q3WDA9_9ACTO	Q3wda9 frankia sp.
36	8	1.8	470	2	Q8EVS9_MYCPE	Q8evs9 mycoplasma
37	8	1.8	494	2	Q8PUI9_METMA	Q8pui9 methanosarc
38	8	1.8	494	2	Q8PUI6_METMA	Q8pui6 methanosarc
39	8	1.8	494	2	Q8PXB4_METMA	Q8pxb4 methanosarc
40	8	1.8	494	2	Q8TRX0_METAC	Q8trx0 methanosarc
41	8	1.8	494	2	Q8TTG5_METAC	Q8ttg5 methanosarc
42	8	1.8	497	2	Q8TIC8_METAC	Q8tic8 methanosarc
43	8	1.8	497	2	Q8TMH9_METAC	Q8tmh9 methanosarc
44	8	1.8	509	2	Q2XIQ6_9GAMM	Q2xig6 shewanella
45	8	1.8	509	2	Q2ZSR6_SHEPU	Q2zsr6 shewanella

ALIGNMENTS

RESULT 1
Q9L8S4_HELPPY PRELIMINARY; PRT; 462 AA.
AC Q9L8S4; integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 2.
DT 01-JUN-2003, entry version 17.
DE Alpha-1,3/4-fucosyltransferase.
GN Name=fucTa;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RX MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RT "Cloning and characterization of the alpha(1,3/4) fucosyltransferase
of Helicobacter pylori".
RL J. Biol. Chem. 275:4988-4994(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UA948;
RA Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; GlycoTrans_10; 1.
KW Glycosyltransferase; transferase.
SQ SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;

Query Match	100.0%;	Score 456;	DB 2;	Length 462;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MFQPLDAPIDSTHLDTHKPPPLNVALANWPLKNSEKKGFRDFILHLFKQRYKIILH	60	
Db	1	MFQPLDAPIDSTHLDTHKPPPLNVALANWPLKNSEKKGFRDFILHLFKQRYKIILH	60	
QY	61	SNPNPESDLVFGNPLEQARKILSYQNTKRVFTGENEVFNFLFDYAIGFDELDNDRYL	120	
Db	61	SNPNPESDLVFGNPLEQARKILSYQNTKRVFTGENEVFNFLFDYAIGFDELDNDRYL	120	
QY	121	RMPLYAVLHYKAMLVNDTTSYKLLKALYTLKPKSHKFKENHPNLCALIHNSDPPKRGF	180	

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Db 121 RMPLYAYLHYKAMLVNDTTSYKALALYTLKKPSHKFKENHPNLCAIHNESDPWKRGF 180
Qy 181 ASFVSNPNAPINAFYDALNATEPVASGGSVKNTLGKVKKNKNEFLSOYKFNLCFENSQ 240
Db 181 ASFVSNPNAPINAFYDALNATEPVASGGSVKNTLGKVKKNKNEFLSOYKFNLCFENSQ 240
Qy 241 GYGVTTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLHAQN 300
Db 241 GYGVTTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNFDIAIDYIRYLHAQN 300
Qy 301 AYLDMLYENPLNTIDGKAGFYQDLSPFKILDFFKNILNDTIYHCNDHAHYSALHRDLNEP 360
Db 301 AYLDMLYENPLNTIDGKAGFYQDLSPFKILDFFKNILNDTIYHCNDHAHYSALHRDLNEP 360
Qy 361 LVSVDLRRDHDLDLVNYYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRDHDLDLRDH 420
Db 361 LVSVDLRRDHDLDLVNYYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRDHDLDLRDH 420
Qy 421 ERLLSKATPULLELSQNTSPFKIYKAYOKSLPLLRAI 456
Db 421 ERLLSKATPULLELSQNTSPFKIYKAYOKSLPLLRAI 456

RESULT 2
Q6ST35_HELPY
ID Q6ST35_HELPY PRELIMINARY; PRT; 432 AA.
AC Q6ST35;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Alpha-1,4 fucosyltransferase.
GN Name=fucTIII;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 6709; DOI=10.1093/glycob/cwj004;
RX PubMed=16006696; Miska V., Wipf B., Ernst B.;
RT "Molecular Cloning and Functional Expression of a Novel Helicobacter
RT pylori (alpha)-1,4 Fucosyltransferase.";
RL Glycobiology 15:1076-1083(2005).
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CC -----
CC EMBL; AY450598; AAR88243.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11329; Glyco_trans_10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 432 AA; 50503 MW; 69D3A32PBD2F12C9 CRC64;

Query Match 15.6%; Score 71; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.7e-63;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 VKKNNEFLSQYKFNLCFENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNV 279
Db 218 VKKNNEFLSQYKFNLCFENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNV 277
Qy 280 HDFNFDIAID 290
Db 278 HDFNFDIAID 288

RESULT 3
Q25142_HELPY
ID Q25142_HELPY PRELIMINARY; PRT; 425 AA.
AC Q25142;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Fucosyltransferase.
GN OrderedLocusNames=HP0379; ORFNames=HP_0379;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McInerney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
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CC -----
CC EMBL; AE000511; AAD07447.1; -; Genomic_DNA.
DR PIR; C64567; C64567.
DR TIGR; HP0379; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco_trans_10.
DR PANTHER; PTHR11329; Glyco_trans_10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;

Query Match 14.9%; Score 68; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 7.5e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 BFLSQYKFNLCFENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 BFLSQYKFNLCFENSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 4
Q25366_HELPY
ID Q25366_HELPY PRELIMINARY; PRT; 476 AA.
AC Q25366;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Fucosyltransferase.
GN OrderedLocusNames=HP0651; ORFNames=HP_0651;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
```

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen *Helicobacter*
RT *pylori*.";
RL Nature 388:539-547(1997).
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CC -----
DR EMBL; AE000511; AAD07710.1; -, Genomic_DNA.
DR PIR; C64601; C64601.
DR TIGR; HP0651; -.
DR LinkHub; O25366; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
KW NCBI_TaxID=85963;
SQ SEQUENCE 476 AA; 55927 MW; 32BFEBB36ELF74 CRC64;

Query Match 14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.3e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 EFLSQYKFLCFNSQGYVTEKILDAYSHHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFLCFNSQGYVTEKILDAYSHHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

Qy 285 FDEALDIYI 292
Db 288 FDEALDIYI 295

RESULT 5
O32631_HELPY PRELIMINARY; PRT; 333 AA.
AC O32631;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-).
GN Name=fuct;
OS *Helicobacter pylori* (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97407924; PubMed=92611148; DOI=10.1074/jbc.272.34.21349;
STRAIN=NCCTC 11637;
RA Martin S.L., Edbrooke M.R., Hodgman T.C., van den Bijnden D.H.,
RA Bird M.I.;
RT "Lewis X biosynthesis in *Helicobacter pylori*. Molecular cloning of an
RT alpha(1,3)-fucosyltransferase gene.";
RL J. Biol. Chem. 272:21349-21356(1997).
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CC -----
DR EMBL; AF006039; AAB93985.1; -, Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.

DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 333 AA; 39154 MW; CFFCB1AC127E0A8C CRC64;

Query Match 9.0%; Score 41; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEALDIY 291
Db 132 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNNFDEALDIY 172

RESULT 6
O9ZLI3_HELPJ PRELIMINARY; PRT; 454 AA.
ID O9ZLI3_HELPJ
AC O9ZLI3;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.
GN Name=fuct; ORFNames=jhp_0596;
OS *Helicobacter pylori* J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen *Helicobacter pylori*.";
RL Nature 397:176-180(1999).
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DR EMBL; AE001439; AAD06169.1; -, Genomic_DNA.
DR PIR; B71914; B71914.
DR Biocyc; HPYL85963:JHP0596-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
KW NCBI_TaxID=454 AA; 53448 MW; 3262687131263AB0 CRC64;
SQ SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;

Query Match 8.6%; Score 39; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 410
Db 364 DDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDL 402

RESULT 7
O9ZKD7_HELPJ PRELIMINARY; PRT; 436 AA.
ID O9ZKD7_HELPJ
AC O9ZKD7;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE ALPHA-(1,3)-FUCOSYLTRANSFERASE.
GN Name=fuct; ORFNames=jhp_1002;
OS *Helicobacter pylori* J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
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CC
CC EMBL; AB001439; AAD06573.1; -; Genomic_DNA.
DR PIR; G71862.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 436 AA; 50699 MW; 1DB2066AE98FA61E CRC64;

Query Match 8.3%; Score 38; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.9e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ARKILSYQNTKRVYTCGENEVPNPNLFDYAIGFDELDF 115
DB [|||||]|||||
78 ARKILSYQNTKRVYTCGENEVPNPNLFDYAIGFDELDF 115

RESULT 8
O30511 HELPY
ID O30511 HELPY PRELIMINARY; PRT; 478 AA.
AC O30511;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Alpha1,3-fucosyltransferase.
GN Name=fucT;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11639;
RX MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
RA Ge Z., Chan N.W.C., Palfic M.M., Taylor D.E.;
RT "Cloning and heterologous expression of an alpha1,3-fucosyltransferase
RT gene from the gastric pathogen Helicobacter pylori.";
RL J. Biol. Chem. 272:21357-21363(1997).
CC
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CC
CC EMBL; AF008596; AAB81031.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008417; F:fucosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001503; Glyco trans 10.
DR PANTHER; PTHR11929; Glyco trans 10; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;

Query Match 7.0%; Score 32; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DAYFSHTPIYWGSPSVAKDFNPKSFVNVDHF 282
DB [|||||]|||||
253 DAYFSHTPIYWGSPSVAKDFNPKSFVNVDHF 284

RESULT 9
Q9FDN3_BACFR
ID Q9FDN3_BACFR PRELIMINARY; PRT; 308 AA.
AC Q9FDN3;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Redox-sensitive transcriptional activator OxyR.
GN Name=oxyR;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IB263;
RX MEDLINE=20416215; PubMed=10960088;
RX DOI=10.1128/JB.182.18.5059-5069.2000;
RA Rocha E.R., Owens G. Jr., Smith C.J.;
RT "The redox-sensitive transcriptional activator OxyR regulates the
RT peroxide response regulon in the obligate anaerobe Bacteroides
RT fragilis.";
RL J. Bacteriol. 182:5059-5069(2000).
CC -!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
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CC
CC EMBL; AF206034; AAG02620.1; -; Genomic_DNA.
DR HSSP; P11721; 1169.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH LysR.
DR InterPro; IPR005119; LysR subst bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS50931; HTHLYSR; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 308 AA; 35190 MW; 2A69F365C77A949F CRC64;

Query Match 2.0%; Score 9; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 LEQARKILS 83
DB [|||||]|||||
65 LEQARKILS 73

RESULT 10
Q5LFO8_BACFN
ID Q5LFO8_BACFN PRELIMINARY; PRT; 308 AA.
AC Q5LFO8;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Redox-sensitive transcriptional activator.
GN Name=oxyR; OrderedLocustName=BF1318;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.

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OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Croseman L.C., Blakely G.,
RA Abratt V., Lennard N., Foxton I., Guerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertcrak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.,
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465 (2005).
CC -!- SIMILARITY: Contains 1 HTH lyseR-type DNA-binding domain.
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CC
CC EMBL; CR626927; CAH07035.1; -; Genomic DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH_LySR.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH_1; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00931; HTH_LYSR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 308 AA; 35248 MW; B3AD6095FB895BA3 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 308;
Best Local Similarity 100.0%; Pred.No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 LEQARKILS 83
Db 65 LEQARKILS 73

RESULT 11
Q9FDN4 BACFR PRELIMINARY; PRT; 308 AA.
AC Q9FDN4
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Redox-sensitive transcriptional activator OxyR.
GN Name=oXyR; OrderedLocusNames=BF1334;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=638R;
RX MEDLINE=20416215; PubMed=10960088;
RX DOI=10.1128/JB.182.18.5059-5069.2000;
RA Rocha E.R., Owens G. Jr., Smith C.J.;
RT "The redox-sensitive transcriptional activator OxyR regulates the
RT peroxide response regulon in the obligate anaerobe Bacteroides
RT fragilis.";
RL J. Bacteriol. 182:5059-5069 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
CC -!- SIMILARITY: Contains 1 HTH lyseR-type DNA-binding domain.
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CC
CC EMBL; AF206033; AAG02619.1; -; Genomic DNA.
DR EMBL; AP008841; BAD48083.1; -; Genomic DNA.
DR HSSP; P11721; 1169.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH_LySR.
DR InterPro; IPR005119; LyseR_subst_bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH_1; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00931; HTH_LYSR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 308 AA; 35248 MW; B3AD6095FB895BA3 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 308;
Best Local Similarity 100.0%; Pred.No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 LEQARKILS 83
Db 65 LEQARKILS 73

RESULT 12
Q8FR14 COREF PRELIMINARY; PRT; 151 AA.
AC Q8FR14
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Putative large-conductance mechanosensitive channel protein.
GN OrderedLocusNames=CE0953;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
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CC
CC EMBL; BA000035; BAC17763.1; -; Genomic DNA.
DR HSSP; 053898; 1MSL.
DR BioCyc; CEPF196164:CE0953-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001185; MS_channel.
DR Pfam; PF01741; MscL; 1.
DR PRINTS; PR01264; MECHCHANNEL.
DR ProDom; PD007253; MS_Channel; 1.
DR TIGRFAMs; TIGR00220; mscL; 1.
KW Complete proteome.
SQ SEQUENCE 151 AA; 16067 MW; 2BCABED7A77BD37 CRC64;

Query Match 1.8%; Score 8; DB 2; Length 151;
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 KGRDFIL 47
DB 3 KGRDFIL 10

RESULT 13
Q34YL2_9GAMM
ID Q34YL2_9GAMM PRELIMINARY; PRT; 154 AA.
AC Q34YL2;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=MlgDRAFT_1278;
OS Alkalilimnicola ehrlichei MLHE-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Ectothiorhodospiraceae; Alkalilimnicola.
OX NCBI_TaxID=187272;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=MLHE-1;
RC US DOE Joint Genome Institute (JGI-PGP);
RG Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Alkalilimnicola
RT ehrlichei MLHE-1.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=MLHE-1;
RC US DOE Joint Genome Institute (JGI-ORNL);
RG Larimer F., Land M.;
RA "Annotation of the draft genome of Alkalilimnicola ehrlichei MLHE-1.";
RT Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC EMBL; AALK01000008; EAP34290.1; -; Genomic_DNA.
CC Hypothetical protein.
SQ SEQUENCE 154 AA; 15050 MW; 85FB6AD5F8AD0384 CRC64;

Query Match 1.8%; Score 8; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 PLEQARKI 81
DB 13 PLEQARKI 20

RESULT 14
Q8XY28_RALSO
ID Q8XY28_RALSO PRELIMINARY; PRT; 159 AA.
AC Q8XY28;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE PROBABLE BACTERIOPHAGE PROTEIN.
GN OrderedLocNames=RSC1935; ORFNames=RS03504;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=GM1000;
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RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
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CC
CC EMBL; AL646067; CAD15637.1; -; Genomic_DNA.
DR BiOCYC; RSC1935-MONOMER; -.
DR GO; GO:0019069; P:viral capsid assembly; IEA.
DR InterPro; IPR009225; Phage_GPL.
DR Pfam; PF05926; Phage_GPL; 1.
KW Complete proteome.
SQ SEQUENCE 159 AA; 17077 MW; 67F13D46A7C90FD3 CRC64;

Query Match 1.8%; Score 8; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 SVDDLRRD 370
DB 133 SVDDLRRD 140

RESULT 15
Q48279_HAESO
ID Q48279_HAESO PRELIMINARY; PRT; 170 AA.
AC Q48279;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Putative capsid completion protein.
OS Haemophilus somnus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Histophilus.
OX NCBI_TaxID=731;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=HS25;
RC MEDLINE=97221585; PubMed=9068631;
RA Pontarollo R.A., Rioux C.R., Potter A.A.;
RT "Cloning and characterization of bacteriophage-like DNA from
RT Haemophilus somnus homologous to phages P2 and HP1.";
RL J. Bacteriol. 179:1872-1879(1997).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=HS25;
RC Pontarollo R.A.;
RA Thesis (1996), V. I. D. O., University of Saskatchewan.
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CC
CC EMBL; U28154; AAC45160.1; -; Genomic_DNA.
DR GO; GO:0019069; P:viral capsid assembly; IEA.
DR InterPro; IPR009225; Phage_GPL.
DR Pfam; PF05926; Phage_GPL; 1.
SQ SEQUENCE 170 AA; 19924 MW; 9D1C2C427A5F20B3 CRC64;

Query Match 1.8%; Score 8; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 SVDDLRRD 370
DB 144 SVDDLRRD 151
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Search completed: August 11, 2006, 20:08:04
Job time : 165.721 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:08:30 ; Search time 31.6006 Seconds
(without alignments)
1263.076 Million cell updates/sec

Title: US-10-764-212-20

Perfect score: 456

Sequence: 1 MFQPLDFAIDSTHLDTH.....TSFKYIKAYOKSLPLRAI 456

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649417

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.psp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.psp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.psp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.psp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.psp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.psp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	14.9	425	2	US-09-092-315-6
2	68	14.9	425	2	US-09-733-524A-6
3	68	14.9	425	2	US-10-189-977A-6
4	68	14.9	425	3	US-10-392-098A-6
5	68	14.9	476	2	US-09-092-315-5
6	68	14.9	476	2	US-09-733-524A-5
7	68	14.9	476	2	US-10-189-977A-5
8	68	14.9	476	3	US-10-392-098A-5
9	41	9.0	454	2	US-09-092-315-8
10	41	9.0	454	2	US-09-733-524A-8
11	41	9.0	454	2	US-10-189-977A-8
12	41	9.0	454	3	US-10-392-098A-8
13	39	8.6	486	2	US-09-092-315-2
14	39	8.6	486	2	US-09-733-524A-2
15	39	8.6	486	2	US-10-189-977A-2
16	39	8.6	486	3	US-10-392-098A-2
17	32	7.0	372	2	US-09-092-315-13
18	32	7.0	440	2	US-09-092-315-3
19	32	7.0	440	2	US-09-733-524A-3
20	32	7.0	440	2	US-10-189-977A-3
21	32	7.0	440	3	US-10-392-098A-3
22	32	7.0	464	2	US-09-092-315-1
23	32	7.0	464	2	US-09-733-524A-1
24	32	7.0	464	2	US-10-189-977A-1
25	32	7.0	464	3	US-10-392-098A-1
26	32	7.0	478	2	US-09-092-315-7

27	32	7.0	478	2	US-09-733-524A-7	Sequence 7, Appli
28	32	7.0	478	2	US-10-189-977A-7	Sequence 7, Appli
29	32	7.0	478	3	US-10-392-098A-7	Sequence 7, Appli
30	16	3.5	36	2	US-09-092-315-14	Sequence 14, Appl
31	16	3.5	36	2	US-09-733-524A-14	Sequence 14, Appl
32	16	3.5	36	2	US-10-189-977A-14	Sequence 14, Appl
33	16	3.5	36	3	US-10-392-098A-14	Sequence 14, Appl
34	13	2.9	502	2	US-10-080-960-16	Sequence 16, Appl
35	8	1.8	515	2	US-09-328-352-5090	Sequence 5090, Ap
36	7	1.5	7	2	US-09-733-524A-25	Sequence 25, Appl
37	7	1.5	7	2	US-10-189-977A-25	Sequence 25, Appl
38	7	1.5	7	3	US-10-392-098A-25	Sequence 25, Appl
39	7	1.5	67	2	US-09-673-395A-167	Sequence 167, App
40	7	1.5	95	2	US-09-328-352-5647	Sequence 5647, Ap
41	7	1.5	116	2	US-09-489-039A-13377	Sequence 13377, A
42	7	1.5	127	2	US-09-902-540-14729	Sequence 14729, A
43	7	1.5	149	2	US-09-252-991A-28856	Sequence 28856, A
44	7	1.5	150	2	US-09-893-737-2	Sequence 2, Appli
45	7	1.5	167	2	US-10-101-464A-664	Sequence 664, App

ALIGNMENTS

RESULT 1
US-09-092-315-6
; Sequence 6, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; PRIORITY FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-6

Query Match 14.9%; Score 68; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 EFLSYKKNLCFNSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
DB 228 EFLSYKKNLCFNSQGYVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287
QY 285 FDEAIDYI 292
DB 288 FDEAIDYI 295

RESULT 2
US-09-733-524A-6
; Sequence 6, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; PRIORITY FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-6

Query Match 14.9%; Score 68; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 3
US-10-189-977A-6
; Sequence 6, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-6

Query Match 14.9%; Score 68; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 4
US-10-392-098A-6
; Sequence 6, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-00042005

; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695B
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-6

Query Match 14.9%; Score 68; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 5
US-09-092-315-5
; Sequence 5, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-5

Query Match 14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYVTEKILDAYFHSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 6
US-09-733-524A-5
; Sequence 5, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:

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; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match          14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 7
US-10-189-977A-5
; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-5

Query Match          14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 8
US-10-392-098A-5
; Sequence 5, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-5

Query Match          14.9%; Score 68; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 9
US-09-092-315-8
; Sequence 8, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-8

Query Match          9.0%; Score 41; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNFDFAIDY 291
Db 253 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNFDFAIDY 293
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; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5

Query Match          14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 7
US-10-189-977A-5
; Sequence 5, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-5

Query Match          14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 8
US-10-392-098A-5
; Sequence 5, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-5

Query Match          14.9%; Score 68; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 9
US-09-092-315-8
; Sequence 8, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-8

Query Match          9.0%; Score 41; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNFDFAIDY 291
Db 253 DAYFSHTPIYWGSPSVAKDFNPKSFVNVHDFNFDFAIDY 293
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RESULT 10
US-09-733-524A-8
; Sequence 8, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-8

Query Match          9.0%; Score 41; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 291
Db 253 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 293

RESULT 11
US-10-189-977A-8
; Sequence 8, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-8

Query Match          9.0%; Score 41; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 291
Db 253 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 293

RESULT 12
US-10-392-098A-8
; Sequence 8, Application US/10392098A
; Patent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; APPLICANT: Universon of Alberta
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REFERENCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/392,098A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 09/733,524
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain NCTC11637
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fuct (HpFuct)
US-10-392-098A-8

Query Match          9.0%; Score 41; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 291
Db 253 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVDHNNFDEAIDY 293

RESULT 13
US-09-092-315-2
; Sequence 2, Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/09/092,315
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: US 60/048,857
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-2

Query Match          8.6%; Score 39; DB 2; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 DDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRL 410
Db 365 DDLRVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRLVNYDDLRL 403

RESULT 14
US-09-733-524A-2
; Sequence 2, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
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; APPLICANT: Taylor, Diane B.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/09/733,524A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-2

Query Match 8.6%; Score 39; DB 2; Length 486;
Best Local Similarity 100.0%; Pred.No. 1.1e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 DDLRVNYYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDLVR 410
Db 365 DDLRVNYYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDL 403

RESULT 15
US-10-189-977A-2
; Sequence 2, Application US/10189977A
; Patent No. 6962806
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane B.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1.3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/189,977A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977A-2

Query Match 8.6%; Score 39; DB 2; Length 486;
Best Local Similarity 100.0%; Pred.No. 1.1e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 DDLRVNYYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDL 410
Db 365 DDLRVNYYDDLVRVYDDLVRVYDDLVRVYDDLVRVYDDL 403

Search completed: August 11, 2006, 20:10:49
Job time : 32.6006 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:09:35 ; Search time 110.092 Seconds
(without alignments)
1918.625 Million cell updates/sec

Title: US-10-764-212-20
Perfect score: 456
Sequence: 1 MFQPLDAFIDSTHLDTH.....TSFKIYKAYQKSLFLRAI 456

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	456	100.0	456	5	US-10-764-212-20		Sequence 20, Appl
2	201	44.1	227	5	US-10-764-212-25		Sequence 25, Appl
3	68	14.9	424	3	US-09-733-524-16		Sequence 16, Appl
4	68	14.9	425	4	US-10-120-319-6		Sequence 6, Appl
5	68	14.9	425	4	US-10-189-977-6		Sequence 6, Appl
6	68	14.9	425	4	US-10-392-098-6		Sequence 6, Appl
7	68	14.9	425	5	US-10-764-212-12		Sequence 12, Appl
8	68	14.9	476	3	US-09-733-524-15		Sequence 15, Appl
9	68	14.9	476	4	US-10-120-319-5		Sequence 5, Appl
10	68	14.9	476	4	US-10-189-977-5		Sequence 5, Appl
11	68	14.9	476	4	US-10-392-098-5		Sequence 5, Appl
12	50	11.0	446	5	US-10-764-212-16		Sequence 16, Appl
13	46	10.1	391	5	US-10-764-212-66		Sequence 66, Appl
14	46	10.1	432	5	US-10-764-212-4		Sequence 4, Appl
15	41	9.0	454	3	US-09-733-524-18		Sequence 18, Appl
16	41	9.0	454	4	US-10-120-319-8		Sequence 8, Appl
17	41	9.0	454	4	US-10-189-977-8		Sequence 8, Appl
18	41	9.0	454	4	US-10-392-098-8		Sequence 8, Appl
19	39	8.6	171	5	US-10-764-212-61		Sequence 61, Appl
20	39	8.6	485	3	US-09-733-524-2		Sequence 2, Appl
21	39	8.6	485	5	US-10-764-212-6		Sequence 6, Appl
22	39	8.6	486	4	US-10-120-319-2		Sequence 2, Appl
23	39	8.6	486	4	US-10-189-977-2		Sequence 2, Appl
24	39	8.6	486	4	US-10-392-098-2		Sequence 2, Appl
25	39	8.6	486	5	US-10-764-212-2		Sequence 2, Appl
26	38	8.3	421	4	US-10-335-977-8558		Sequence 8558, Ap
27	38	8.3	436	4	US-10-335-977-8559		Sequence 8559, Ap

28	36	7.9	377	5	US-10-764-212-68	Sequence 68, Appl
29	32	7.0	372	4	US-10-120-319-13	Sequence 13, Appl
30	32	7.0	372	4	US-10-189-977-13	Sequence 13, Appl
31	32	7.0	440	4	US-10-120-319-3	Sequence 3, Appl
32	32	7.0	440	4	US-10-189-977-3	Sequence 3, Appl
33	32	7.0	440	4	US-10-392-098-3	Sequence 3, Appl
34	32	7.0	440	5	US-10-764-212-18	Sequence 18, Appl
35	32	7.0	464	4	US-10-120-319-1	Sequence 1, Appl
36	32	7.0	464	4	US-10-189-977-1	Sequence 1, Appl
37	32	7.0	464	4	US-10-392-098-1	Sequence 1, Appl
38	32	7.0	478	4	US-10-120-319-7	Sequence 7, Appl
39	32	7.0	478	4	US-10-189-977-7	Sequence 7, Appl
40	32	7.0	478	4	US-10-392-098-7	Sequence 7, Appl
41	32	7.0	479	3	US-09-733-524-17	Sequence 17, Appl
42	29	6.4	247	5	US-10-764-212-73	Sequence 73, Appl
43	28	6.1	245	5	US-10-764-212-72	Sequence 72, Appl
44	28	6.1	247	5	US-10-764-212-76	Sequence 76, Appl
45	28	6.1	256	5	US-10-764-212-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-10-764-212-20
; Sequence 20, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 948 PutA fucosyltransferase
US-10-764-212-20

Query Match	100.0%	Score 456;	DB 5;	Length 456;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches	456;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MFQPLDAFIDSTHLDTHKPLNVALANWWPLKNSKKGFRDPLHFLHKQYKILH	60	
Db	1	MFQPLDAFIDSTHLDTHKPLNVALANWWPLKNSKKGFRDPLHFLHKQYKILH	60	
QY	61	SNPNPSDLVFGNPLQARKILSYQNTKRVYTTGENEVPNFNLDYAGDELDNDRYL	120	
Db	61	SNPNPSDLVFGNPLQARKILSYQNTKRVYTTGENEVPNFNLDYAGDELDNDRYL	120	
QY	121	RMPLYAYLHYKAMLVNDTTSVKLALYTLKPKSHKFKENHPNLCALIHNSDPWKRGF	180	
Db	121	RMPLYAYLHYKAMLVNDTTSVKLALYTLKPKSHKFKENHPNLCALIHNSDPWKRGF	180	
QY	181	ASFVSNPNAPIRNAPYDALNAIEPVASGSGVNTLGYKVKKNKNEFLSQYKFNLCFENSQ	240	
Db	181	ASFVSNPNAPIRNAPYDALNAIEPVASGSGVNTLGYKVKKNKNEFLSQYKFNLCFENSQ	240	
QY	241	GYGYVTEKILDYFSTHTPIYNGSPSVAKDFNPKSPVNVHDFNFDIAIDYIRYLHAQN	300	
Db	241	GYGYVTEKILDYFSTHTPIYNGSPSVAKDFNPKSPVNVHDFNFDIAIDYIRYLHAQN	300	
QY	301	AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHDLNLP	360	

Db 301 AYLDMLYENFLATIDGKAGFYQDLSFEKILDPFKNILENTDIYHCNDAHYSALHRDLNEP 360
Qy 361 LVSVDLRRDHDLDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRDHDLDLRDH 420
Db 361 LVSVDLRRDHDLDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRDHDLDLRDH 420
Qy 421 ERLLSKATPLLELSQNTSEFKLYRKAYOKSLPLLRAI 456
Db 421 ERLLSKATPLLELSQNTSEFKLYRKAYOKSUPLLRAI 456

RESULT 2

US-10-764-212-25

; Sequence 25, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H. pylori
; OTHER INFORMATION: strain 955 FutA fucosyltransferase coding
; OTHER INFORMATION: sequence amino acid translation peptide

US-10-764-212-25

Query Match 44.1%; Score 201; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 49 FILKQRYKIILHSPNEPSDLVFGNPLQOARKILSYQNTKRVFTGNEVFNFLFDYAI 108
Db 26 FILKQRYKIILHSPNEPSDLVFGNPLQOARKILSYQNTKRVFTGNEVFNFLFDYAI 85
Qy 109 GFDELDFNDRLRMPLYYAYILHYKAMLVNDTTPSYKLKALYTLKKPSHKFKENHPNLCAL 168
Db 86 GFDELDFNDRLRMPLYYAYILHYKAMLVNDTTPSYKLKALYTLKKPSHKFKENHPNLCAL 145
Qy 169 IHNESDPKRGFASFVSNPNAPIRNAPFYDALNAIEPVASGSGVKNTLGYKVKKNFELS 228
Db 146 IHNESDPKRGFASFVSNPNAPIRNAPFYDALNAIEPVASGSGVKNTLGYKVKKNFELS 205
Qy 229 QYKFNLCFENSQGYGYVTEKI 249
Db 206 QYKFNLCFENSQGYGYVTEKI 226

RESULT 3

US-09-733-524-16

; Sequence 16, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524

; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695B
US-09-733-524-16

Query Match 14.9%; Score 68; DB 3; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.3e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 225 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 4

US-10-120-319-6

; Sequence 6, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-6

Query Match 14.9%; Score 68; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 225 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 5

US-10-189-977-6

; Sequence 6, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming

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; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-6

Query Match      14.9%; Score 68; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 6
US-10-392-098-6
; Sequence 6, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-6

Query Match      14.9%; Score 68; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 7
US-10-764-212-12
; Sequence 12, Application US/10764212
; Publication No. US20050164338A1
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; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 26695 Puta fucosyltransferase
US-10-764-212-12

Query Match      14.9%; Score 68; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287

QY 285 FDEAIDYI 292
Db 288 FDEAIDYI 295

RESULT 8
US-09-733-524-15
; Sequence 15, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)---(0)
; OTHER INFORMATION: Strain 26695A
US-09-733-524-15

Query Match      14.9%; Score 68; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 284
Db 228 EFLSQYKFNLCFNSQGYGVTEKILDAYFSHTIPIYWGSPSVAKDNPFSFVNVHDFNN 287

QY 285 FDEAIDYI 292
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Db      288 FDEAIDYI 295
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RESULT 9
US-10-120-319-5
; Sequence 5, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-5

Query Match      14.9%; Score 68; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db      228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy      285 FDEAIDYI 292
Db      288 FDEAIDYI 295

RESULT 10
US-10-189-977-5
; Sequence 5, Application US/10189977
; Publication No. US20030168211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-5

Query Match      14.9%; Score 68; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db      228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy      285 FDEAIDYI 292
Db      288 FDEAIDYI 295

RESULT 11
US-10-392-098-5
; Sequence 5, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; FILE REFERENCE: 07254-049002
; CURRENT APPLICATION NUMBER: US/10/392,098
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US/09/733,524A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-5

Query Match      14.9%; Score 68; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
Db      228 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
Qy      285 FDEAIDYI 292
Db      288 FDEAIDYI 295

RESULT 12
US-10-764-212-16
; Sequence 16, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 FutB fucosyltransferase
US-10-764-212-16

Query Match      11.0%; Score 50; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.7e-38;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      225 EFLSQYKFNLCFENSQGYGVTEKILDAYFSHTTIPIYWGSPSVAKDFNPK 274
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Db 227 EFSLQKFNLCFNSQGYGVVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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RESULT 13

US-10-764-212-66
; Sequence 66, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Daniel F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 Puta fucosyltransferase
; OTHER INFORMATION: catalytic domain conserved region positions 27-417
US-10-764-212-66

Query Match 10.1%; Score 46; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 9.4e-35; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
|||||

Db 226 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 271
|||||

RESULT 14

US-10-764-212-4
; Sequence 4, Application US/10764212
; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Johnson, Karl F.
; APPLICANT: Bezila, Daniel James
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; OTHER INFORMATION: H. pylori strain 1111 Puta fucosyltransferase
US-10-764-212-4

Query Match 10.1%; Score 46; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-34; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
|||||

Db 252 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 297
|||||

RESULT 15

US-09-733-524-18
; Sequence 18, Application US/09733524
; Patent No. US20020068347A1
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 454
; TYPE: PRT
; ORGANISM: helicobacter pylori fucosyltransferase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)---(0)
; OTHER INFORMATION: Strain 11637 from NCTC11637
US-09-733-524-18

Query Match 9.0%; Score 41; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 5.9e-30; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 0;

Qy 251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDY 291
|||||

Db 253 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDY 293
|||||

Search completed: August 11, 2006, 20:16:18
Job time : 111.092 secs

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OM protein - protein search, using sw model

Run on: August 11, 2006, 20:11:06 ; Search time 17.3294 Seconds
(without alignments)
1771.230 Million cell updates/sec

Title: US-10-764-212-20
Perfect score: 456
Sequence: 1 MFQPLDAPIDSTHLETH.....TSFKYRKAYQKSLPLRAI 456

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 239914 seqs, 67312017 residues

Word size : 1

Total number of hits satisfying chosen parameters: 239854

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 - 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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 - 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.5	238	6	US-10-449-902-31893
2	7	1.5	238	6	US-10-449-902-47233
3	7	1.5	245	6	US-10-953-349-25102
4	7	1.5	245	6	US-10-953-349-37062
5	7	1.5	245	6	US-11-056-355B-57749
6	7	1.5	259	6	US-10-953-349-26636
7	7	1.5	259	7	US-11-056-355B-67711
8	7	1.5	276	6	US-10-953-349-26635
9	7	1.5	276	6	US-11-056-355B-67710
10	7	1.5	304	6	US-10-449-902-35964
11	7	1.5	313	6	US-10-953-349-25101
12	7	1.5	313	6	US-10-953-349-37061
13	7	1.5	313	7	US-11-056-355B-57748
14	7	1.5	321	6	US-10-953-349-25100
15	7	1.5	321	7	US-11-056-355B-57747
16	7	1.5	335	6	US-10-953-349-37060
17	7	1.5	350	7	US-11-056-355B-45929
18	7	1.5	350	7	US-11-056-355B-46227
19	7	1.5	350	7	US-11-056-355B-46491
20	7	1.5	350	7	US-11-056-355B-47261
21	7	1.5	350	7	US-11-056-355B-97334
22	7	1.5	350	7	US-11-056-355B-102108
23	7	1.5	350	7	US-11-056-355B-113347
24	7	1.5	377	6	US-10-449-902-40119
25	7	1.5	396	7	US-11-056-355B-45928

26	7	1.5	396	7	US-11-056-355B-46490	Sequence 46490, A
27	7	1.5	396	7	US-11-056-355B-47260	Sequence 47260, A
28	7	1.5	399	7	US-11-056-355B-46226	Sequence 46226, A
29	7	1.5	399	7	US-11-056-355B-102107	Sequence 102107, A
30	7	1.5	399	7	US-11-056-355B-113346	Sequence 113346, A
31	7	1.5	402	6	US-10-553-436-240	Sequence 240, App
32	7	1.5	422	1	US-09-797-238-17	Sequence 17, Appl
33	7	1.5	436	7	US-11-056-355B-46225	Sequence 46225, A
34	7	1.5	436	7	US-11-056-355B-102106	Sequence 102106, A
35	7	1.5	436	7	US-11-056-355B-113345	Sequence 113345, A
36	7	1.5	440	6	US-10-953-349-7497	Sequence 7497, Ap
37	7	1.5	547	6	US-10-449-902-54651	Sequence 54651, A
38	7	1.5	578	6	US-10-449-902-31247	Sequence 31247, A
39	7	1.5	578	6	US-10-449-902-50578	Sequence 50578, A
40	7	1.5	667	7	US-11-289-102-250	Sequence 250, App
41	7	1.5	690	6	US-10-449-902-54835	Sequence 54835, A
42	7	1.5	695	7	US-11-330-403-7874	Sequence 7874, Ap
43	7	1.5	801	7	US-11-330-403-14742	Sequence 14742, A
44	7	1.5	1126	6	US-10-449-902-52674	Sequence 52674, A
45	6	1.3	25	7	US-11-134-871-749	Sequence 749, App

ALIGNMENTS

RESULT 1
US-10-449-902-31893
; Sequence 31893, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31893
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31893

Query Match 1.5%; Score 7; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 DLNEPLV 362
DB 9 DLNEPLV 15
|||||

RESULT 2
US-10-449-902-47233
; Sequence 47233, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47233
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47233

Query Match 1.5%; Score 7; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 DLNEPLV 362
| | | | |
Db 9 DLNEPLV 15

RESULT 3

US-10-953-349-25102
; Sequence 25102, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25102
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-25102

Query Match 1.5%; Score 7; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
| | | | |
Db 195 PLNVALA 201

RESULT 4

US-10-953-349-37062
; Sequence 37062, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37062
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37062

Query Match 1.5%; Score 7; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
| | | | |

Db 195 PLNVALA 201

RESULT 5

US-11-056-355B-57749
; Sequence 57749, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 57749
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; NAME/KEY: peptide
; LOCATION: (1)..(245)
; OTHER INFORMATION: Ceres Seq. ID no. 14316381
US-11-056-355B-57749

Query Match 1.5%; Score 7; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
| | | | |
Db 195 PLNVALA 201

RESULT 6

US-10-953-349-26636
; Sequence 26636, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26636
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26636

Query Match 1.5%; Score 7; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 449 SLPLIRA 455
| | | | |
Db 14 SLPLIRA 20

RESULT 7

US-11-056-355B-67711
; Sequence 67711, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

;
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67711
; LENGTH: 259
; TYPE: prt
; ORGANISM: Triticum aestivum
;
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(259)
; OTHER INFORMATION: Ceres Seq. ID no. 13595883
US-11-056-355B-67711

Query Match 1.5%; Score 7; DB 7; Length 259;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 449 SLPLRA 455
Db 14 SLPLRA 20

RESULT 8
US-10-953-349-26635
; Sequence 26635, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 26635
; LENGTH: 276
; TYPE: prt
; ORGANISM: Triticum aestivum
US-10-953-349-26635

Query Match 1.5%; Score 7; DB 6; Length 276;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 449 SLPLRA 455
Db 31 SLPLRA 37

RESULT 9
US-11-056-355B-67710
; Sequence 67710, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67710
; LENGTH: 276
; TYPE: prt
; ORGANISM: Triticum aestivum

;
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(276)
; OTHER INFORMATION: Ceres Seq. ID no. 13595882
US-11-056-355B-67710

Query Match 1.5%; Score 7; DB 7; Length 276;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 449 SLPLRA 455
Db 31 SLPLRA 37

RESULT 10
US-10-449-902-35964
; Sequence 35964, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 35964
; LENGTH: 304
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-35964

Query Match 1.5%; Score 7; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 PLEQARK 80
Db 228 PLEQARK 234

RESULT 11
US-10-953-349-25101
; Sequence 25101, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 25101
; LENGTH: 313
; TYPE: prt
; ORGANISM: Glycine max
US-10-953-349-25101

Query Match 1.5%; Score 7; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29

Db 263 PLNVALA 269
|||||

RESULT 12

US-10-953-349-37061
; Sequence 37061, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37061
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37061

Query Match 1.5%; Score 7; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
|||||
Db 263 PLNVALA 269

RESULT 13

US-11-056-355B-57748
; Sequence 57748, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 57748
; LENGTH: 313
; TYPE: prt
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)-(313)
; OTHER INFORMATION: Ceres Seq. ID no. 14316380
US-11-056-355B-57748

Query Match 1.5%; Score 7; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
|||||
Db 263 PLNVALA 269

RESULT 14

US-10-953-349-25100
; Sequence 25100, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25100
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-25100

Query Match 1.5%; Score 7; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
|||||
Db 271 PLNVALA 277

RESULT 15

US-11-056-355B-57747
; Sequence 57747, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 57747
; LENGTH: 321
; TYPE: prt
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)-(321)
; OTHER INFORMATION: Ceres Seq. ID no. 14316379
US-11-056-355B-57747

Query Match 1.5%; Score 7; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PLNVALA 29
|||||
Db 271 PLNVALA 277

Search completed: August 11, 2006, 20:17:16
Job time : 19.3294 secs